

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 130245

TO: Jeffrey Parkin

Location: REM-3D39/3E18

Art Unit: 1648

Thursday, September 02, 2004

Case Serial Number: 10/001407

From: Toby Port

Location: Biotech-Chem Library

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Parkin,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port



LING PRICE BLANK (1370)



130245

From:

Parkin, Jeffrey

Sent:

Wednesday, August 18, 2004 10:16 PM

To:

STIC-Biotech/ChemLib

Subject:

Sequence Search: U.S. Serial No. 10/001,407

Please search SEQ ID NOS.: 10 and 15 from U.S. Serial No. 10/001,407 (Yang, Y., and T. Burrell) v. all relevant databases, including interference. SEQ ID NO.: 10 corresponds to a region of the HIV-2 genome so it will probably pick up a large number of full-length sequences. Can you limit the search results to pick up ONLY nucleic acid sequences that are =<100 nucleotides in length for both sequences?

Place results on both disk and paper.

Thanks!

JSP REM 3D39 AU 1648 2-0908

STAFF USE ONLY
Searcher:
Searcher Phone: 2-
Date Searcher Picked up:
Date Completed:
Searcher Prep/Rev. Time:
Online Time:

Type of Search
NA Sequence: #
AA Sequence :#
Structure: #
Bibliographic:
Litigation:
Patent Family:
Other:

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Copyright (c) 1993 - 2004 Compugen Ltd.
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REFERENCE AUTHORS TITLE

lentivirus group.

Yang, Y.Y. and Burrell, T.A. Compositions and methods for detecting human immunodeficiency virus 2 (hiv-2)

Human immunodeficiency virus 2 (HIV-2) Human immunodeficiency virus 2 Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                         Patent: WO 0234951-A 9 02-MAY-2002;
Gen-Probe Incorporated (US)
Location/Qualifiers
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Compositions and methods for detecting
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Human immunodeficiency virus 2
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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Human immunodeficiency virus 2
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                  /organism="Human immunodeficiency virus /mol_type="unassigned DNA" /db_xref="taxon:11709"
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be Incorporated (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:11709"
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1 (bases 1 to 88)
Whitcomb.J.M. and Hughes,S.H.
The sequence of human immunodeficiency virus type 2 circle junction suggests that integration protein cleaves the ends of linear DNA asymmetrically
J. Virol. 65 (7), 3906-3910 (1991)
                                                                                                                                                                                                                    M74763.1 GI:327981

long terminal repeat (LTR).

Human immunodeficiency virus 2 (HIV-2)

Human immunodeficiency virus 2

Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
                                                                  Original source text: Human immunodeficiency Location/Qualifiers
                                                                                                                                                                                                                                                                                                         88 bp DNA linear VRL 02-AUG-1
partial sequence, clone 1.
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/proviral
/mol_type="genomic DNA"
/db_xref="taxon:11709"
                                    organism="Human immunodeficiency"
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/mol_type="unassigned DNA"
/mb_type="unassigned DNA"
/mb_tref="taxon:32630"
/note="T7 promoter primer having a promoter sequence
appended at the 5' end of an HIV-2 complementary primer sequence"
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Gaps

0

VRL 02-AUG-1993

virus type

Length Indels

52

primer

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SOURCE
ORGANISM
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AX498426
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AX498431
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Best Local Similarity
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Best Local !
Query Match
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                                                                                                                                                                                                                                                                               Sequence 19 from Patent AX498431
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                                                                                                                                                                                                                                                                                                                                                                                            1 CGGGCGCCAACCTGCTAG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 2
Human immunodeficiency virus 2
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                                                                                                                                Patent: WO 0234951-A 19 02-MAY-2002;
Gen-Probe Incorporated (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent: WO 0234951-A 14 02-MAY-2002;
Gen-Probe Incorporated (US)
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                                                                                                                                                                                                                                                                                                       AX498431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX498426
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Compositions and methods for detecting human
                                                                                                                                                                                                                                 synthetic
                                                                                                                                                                                                                                           synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entivirus group.
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                                                                                                                                                                      (hiv-2
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                                                          /note="T7 promoter primer having a
appended at the 5' end of an HIV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Human immunodeficiency virus
/mol_type="unassigned DNA"
/db_xref="taxon:11709"
                                               sequence"
                                                                                organism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"
                                                                                                                                                                                                                                 construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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72.0%;
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Pred. No.
Score 18;
Pred. No.
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...d. No. 6e+02;
Mismatches
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WO0234951.
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WO0234951.
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1.9e+03;
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Query Match
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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JOURNAL
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Best Local
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                                                                                          source
                                                                                                                 Is 1 (bases 1 to 22)

Is John, W.B., Suzan, M.A., Ann, E.K., Eric, B.R. and Thomas, J.K.

Amplification and detection of HIV-1 and/or HIV-2

Amplification and detection of HIV-1 and/or HIV-2

Patent: JP 199069987-A, 31 16-MAR-1999;

ORTHO CLINICAL DIAGNOSTICS INC

ON Unidentified

PN UP 1999069987-A/31

PD 16-MAR-1999

PP 24-JUN-1998 JP 1998177059

PR 25-JUN-1997 US 60/050759

PR 25-JUN-1997 US 60/050759

PI JOHN WESLEY BACCHUS, SUZAN MERISSA ATTWOOD, ANN ELIZABETH 1

PR 25-JUN-1997 US 60/050759

PC C12N15/09,C12Q1/68,G01N33/566,G01N33/569,C12N15/00 CC

Strandedness: Single;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

FT source /organism='Unidentified'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41
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AR093423
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                 unidentified
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Backus, J.W., Atwood, S.M., Casey, A.E.,
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ilarity 100.0%;
Conservative
                                                                                                                                                                                        24-JUN-1998 JP 1998177059
55-JUN-1997 US 60/050759
JOHN WESLEY BACCHUS, SUZAN MERISSA ATTWOOD, ANN ELIZABETH ERIC BRICE RASMUSSEN, THOMAS JOSEPH KAMINZU C12N15/09,C12Q1/68,G01N33/566,G01N33/569,C12N15/00 CC
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                                          /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                  /organism='Unidentified'
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:13025679
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68.0%;
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Pred. No.
Score 17;
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6
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Length 22;
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Synthetic construct

artificial sequences.

E 1 (bases 1 to 32)

S Shinohara, K., Sakai, K. and Honda, M.

Nonhuman primatal model of acquired immunodeficiency syndrome patent; JP 2002159296-A 7 04-JUN-2002;

DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES, THE DIRECTOR GENERAL OF PARMACEUTICAL SAFETY AND RESEARCH

OS Artificial Sequence
PN JP 2002159296-A/7

PD 04-JUN-2002
PP 27-NOV-2000 JP 2000360274
PI KATSUAKI SHINOHARA, KOJI SAKAI, MITSUO HONDA
PC C12N15/09, A01K67/027, C12N7/00, C12N7/02, G01N33/15, G01N33/569,
PC G01N33/569, A01K67/027, C12N7/02, C12N15/00 CC
Description of Artificial Sequence: artificially synthesized CC
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Compositions and methods for detecting
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Sequence 13 from Patent
AX498425
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                                                                                                                                       27-NOV-2000 JF 2000360274

KATSUAKI SHINOHARA, KOJI SAKAI, MITSUO HONDA

Cl2N15/09, A01K67/027, C12N7/00, C12N7/02, G01N33/15, G01N33/50//
                           /organism='Artificial Sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO 0234951-A 13 02-MAY-2002; be Incorporated (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer mismatches HIV-2 sequence by
nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Incorporated (US)
Location/Qualifiers
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                                                               Location/Qualifiers
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Pred. No. 1e+04;
0; Mismatches 4; Indels
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Mismatches 0;
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WO0234951,
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Paoletti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K., Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E., Cox,W.I., Audonnet,J.-C.F. and Gettig,R.R.

NYVAC vaccinia virus recombinants comprising heterologous inserts Patent: US 5494807-A 160 27-FEB-1996;
                                                                                                                                                                                                                                                          Unknown.
Unknown.
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I17929
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Unclassified.

1 (bases 1 to 42)

1 (bases 1 to 42)

Paoletti, E., Perkus, M.E., Taylor, J., Tartaglia, J., Nor Riviere, M., de Taisne, C., Limbach, K.J., Johnson, G.P., Cox, W.I., Audonnet, J.-C.Francis. and Gettig, R. Robert. Modified recombinant vaccinia virus and expression vec Patent: US 5762938-A 160 09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Sequence 160 from patent US
AR011291 GI:3969281
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                                                                                             /organism="unknown"
/mol_type="unassigned
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/organism="synthetic co:
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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82.6%;
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patent US 5494807
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Pred. No. 9.7e+03;
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sequence Key

source

REFERENCE AUTHORS TITLE JOURNAL

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VERSION
KEYWORDS

BD161898 Nonhuman BD161898

primatal model

BD161898.1 GI:27867656 JP 2002159296-A/7.

SOURCE ORGANISM

RESULT 11 BD161898 LOCUS

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Query Match Best Local S Matches 19

Similarity

66.4%; ilarity 82.6%; Conservative

19, w

REFERENCE AUTHORS TITLE

FEATURES

Gen-Probe

JOURNAL

KEYWORDS SOURCE ORGANISM

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construct sequences.

artificial

RESULT 10 AX498425 LOCUS

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                                                         Query Match 64.8%; Score 16.2; DB 6; Length 100; Best Local Similarity 85.7%; Pred. No. 1.3e+04; Matches 18; Conservative 0; Mismatches 3; Indels
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64 GGGCGTCAACCTGCAAGGTAT 84
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Sequence 18 from Patent W00234951.
                               N
                                                                                                                                                                                                                              Braun, A., Koester, H., van den Boom, D., Ping, Y., Rodi, C., He, L., Chiu, N. and Jurinke, C.
Methods for generating databases and databases for identifying polymorphic genetic markers
Patent: WO 0127857-A 108 19-APR-2001;
                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                             AX112460 100 bp
Sequence 108 from Patent W00127857.
AX112460
AX112460.1 GI:13939219
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Gen-Probe Incorporated (US)
Location/Qualifiers
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Compositions and methods for detecting human immunodeficiency virus

(hiv-2)
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                  GGGCGCCAACCTGCTAGGGAT 22
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                       (SD)
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Search completed: August 31, 2004, 02:04:24 Job time : 527.623 secs THIS PACE BLANK (USPTO)

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26-AUG-2002
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30-MAR-2001; 2001US-0280058P.
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Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probestarget duplex.

WPI; 2002-489953/52.

Claim 10; Page 25; 58pp; English.

The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a hybridisation probe and detectable label, hybridising HIV-2 NA with the probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the presence of HIV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C with

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The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a combatton probe and detectable label, hybridising HIV-2 NA with the probe to form probe and detectable label, hybridising HIV-2 NA with the considerable to form probe target duplex, and detecting the duplex. The method product such as plasma or serum, and also for detecting subtypes A, B, C and D of HIV-2. The method is useful for amplifying and detecting the NA components of multiplex amplification creactions that synthesise amplicons corresponding to polynucleotides of virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the correspondents of correspondents of the correspondents of t
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Matches 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting human immunodeficiency virus-2 nucleic acids in a sample, amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:
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30-MAR-2001; 2001US-0280058P.
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26-AUG-2002
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Pred. No. 0.011;
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probe:target
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Sequence

34

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4 A;

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10 G;

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                                                                Query Match
Best Local S
Matches 25
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ABK93884/c
ID ABK93884 g
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                  Sequence 34 BP; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 39; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target
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30-MAR-2001; 2001US-0280058P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 2 detection
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26-AUG-2002
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                                                                                    Similarity
CGGGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
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                                                    100.0%; silarity 100.0%; sometive o;
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ilarity 100.0%;
Conservative 0
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(first entry)
                                                                                                                                           A, 10 C;
                                                                                                                                  10 G; 4 T; 0 U; 0 Other;
                                                  Score 25; DB
Pred. No. 0.0
0; Mismatches
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Pred. No. 0.011;
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                                                                           0.011;
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                                                Gaps
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RESULT 5
ABK93890
ID ABK9
XX
AC ABK9
DT 29-A
DT 26-A
XX
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                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                               The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a hybridisation probe and detectable label, hybridising HIV-2 NA with the probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the presence of HIV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C and D of HIV-2. The method is useful for amplifying and detecting the NA in blood serum and also as components of multiplex amplification reactions that synthesise amplicons corresponding to polynucleotides of unrelated viruses, e.g. HIV-1, hepatitis B virus (HEV) and hepatitis C virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target
              29-AUG-2003
26-AUG-2002
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30-MAR-2001; 2001US-0280058P.
                                                            ABK93890;
                                                                                                                                                                                                                                                                                      Sequence 52 BP; 15 A; 11 C; 13 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 25; 58pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV. hepatitis C virus; HCV; probe; ss.
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                                                                                      ABK93890 standard;
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                                                                                                                                                                  28
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                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                  CGGGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                                 CGGGCGCCAACCTGCTAGGGATTTT 52
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(first entry)
              (revised)
(first entry)
                                                                                        DNA;
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                                                                                        ΒP
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                                                                                                                                                                                                                                           Score 25;
Pred. No.
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                                                                                                                                                                                                                                           0.012;
                                                                                                                                                                                                                                                           DB 6;
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RESULT 6
ABK93895
ID ABK9
XX
AC ABK9
XX
AC ABK9
DT 29-A
DT 26-A
DT 26-A
XX
DE Huma
XX
Huma
XX
Huma
XX
OS Huma
XX
PN WO20
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a hybridisation probe and detecting the amplified NA; or providing a probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the presence of HIV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C and D of HIV-2. The method is useful for amplifying and detecting the NA in blood serum and also as components of multiplex amplification reactions that synthesise amplicons corresponding to polynucleotides of unrelated viruses, e.g. HIV-1, hepatitis B virus (HEV) and hepatitis C virus (HCV). ABK93910 represent HIV-2 detection probes of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                            29-AUG-2003
26-AUG-2002
                                                                                                                                                                                                              ABK93895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-489953/52
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30-MAR-2001; 2001US-0280058P.
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                                                                              hepatitis C virus;
                                                                                             Human
                                                                                                                              Human immunodeficiency virus type 2 detection probe #19.
                                                                                                                                                                                                                                              ABK93895 standard; DNA; 58
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                                                                            immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV
itis C virus; HCV; probe; ss.
                                               immunodeficiency virus
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18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                       100.0%; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 C; 7 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                              ВÞ
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                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            6
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WO200234951-A2

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RESULT 7
AAV63697
ID AAV6
XX AAV6
AC AAV6
AC AAV6
XX II-M
DE PCR
XX HIV-
CO-a
XX Synt
CS Humas
PN EP86
XX Synt
XX Synt
CS Humas
XX Synt
XX Syn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                    Backus JW,
                                                    (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
                                                                                                                25-JUN-1997;
                                                                                                                                                               24-JUN-1998;
                                                                                                                                                                                                                 30-DEC-1998.
                                                                                                                                                                                                                                                                EP887427-A2
                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                           HIV-1; HIV-2; detection; Acquired Immunodeficiency Syndrome; AIDS;
co-amplification assay; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV63697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV63697 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 25; 58pp; English.
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30-MAR-2001;
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18; Conserv
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             Atwood SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11arity 100.0%; sc
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 17 A; 17 C; 13 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                           97US-0050759P.
                                                                                                                                                          98EP-00304959
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2001US-0280058P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US045396
                                                                                                                                                                                                                                                                                                                                                                                                                                               amplify HIV-2 sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
       Casey AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
       Rasmussen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
     EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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  Cummins
검
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RESULT 8
ANK93889
YX ABK9
XX ABK9
XX 29-A;
DT 26-A;
XX Huma
XX Huma
XX Huma
XX Huma
XX Hopa
XX
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Best Local
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The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs willst and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a
                                                                                                                                                                 Claim 10; Page
                                                                                                                                                                                                             Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-2000; 2000US-0242620P.
30-MAR-2001; 2001US-0280058P.
                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-489953/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-2001; 2001WO-US045396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200234951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV; hepatitis C virus; HCV; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 2 detection probe #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENP-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-2003
26-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK93889 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present PCR primer is used to amplify human deficiency type 2 (HIV-2) nucleic acids. The specification also describes primers and probes for HIV-1 and HIV-2. The primers and probes are useful for amplifying and biological samples, and for giving propess in our understanding of Acquired Immunodeficiency Syndrome (AIDS). The primers are able to detect all HIV-1 and HIV-2 subtypes without detecting non-related viruses. The primer sets for HIV-1 and HIV-2 are compatible with each other, and can more than one primer ac-amplification assay for HIV-1 and HIV-2. Using overlap a common probe region maximises strain sensitivity and robustness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK93889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 3 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting Human Immunodeficiency Virus 1 and 2 - using at least four new oligonucleotide primers and multiple detection probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-047891/05.
                                                                                                                                                                                                                                                                                                                                                                                                                  Υ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEN-PROBE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGGGCGCCAACCTGCTA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                               Burrell TA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                     58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽₽
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Pred. No. 1.1e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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SSSSSSSSSSSSSSS

hybridisation probe and detectable label, hybridising HIV-2 NA with the probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the presence of HIV-2 NA in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C and D of HIV-2. The method is useful for amplifying and detecting the NA in blood serum and also as components of multiplex amplification reactions that synthesise amplicons corresponding to polynucleotides of unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the invention. (Updated on 29-AUG-2003 to standardise OS field)

유 Ş

N w 19;

GGCGCCAACCTGCTAGGGATTTT 25 GGGCGCCACCTGCTAGGGATTTT 24

AAQ35348;

AAQ35348 standard; DNA;

42

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Query Match Best Local S Matches 19

Similarity

66.4**%**; 82.6**%**;

Conservative

0; Mismatches Score 16.6; DB 6 Pred. No. 1.8e+02 Sequence 24

BP; 3 A;

7 C; 8 G; 6 T; 0 U;

0 Other; DB 6;

Length

Indels

0

Gaps

0

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ARSSULT 9
AAQ3534
ID AAQ353
XX AAQ35
AC AAQ33
XX AAQ35
DT 25-M
DE MUEN
XX Huma
XX Synt
XX Synt
XX Huma
XX Synt
XX Huma
XX Synt
XX Huma
XX Synt
XX Huma
XX FF 11-J
XX Holl
PF 12-J
XX Holl
PF 12-J
XX FF 11-J
XX F
                                  S
                                                                                              Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                        The env gene of HIV was subjected to in vitro mutagenesis to remove the sequences encoding the rex protein and the LTR region from the 3' end of the gene and to delete the putative immuno-suppressive (18) region (amino acids 583-599). Mutagenesis was performed using primers LTR2 and MUENSVISR using pIBI25mutenv8 as template. Mutagenised clones were identified by hybridsation and restriction analyses. See also AAQ35328-437. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-1991;
11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus; HIV; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
18-MAY-1993
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified recombinant virus with inactivated non-essential genetic functions - comprises e.g. vaccine or avipox virus, used as HIV vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paoletti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUENSVISR, a mutagenesis primer for env gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-018128/02
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                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u
T
                                                                                                                          Similarity
GGGCGCCAACCTGCTAGGGATTT
                                                                                                                                                                                                                   42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 49; 159pp; English.
                                                                                                                                                                                                                   BP;
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91US-00715921.
92US-00897382.
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                                                                                                                                                                                                                   A.
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                                                                                                                       66.4%;
                                                                                                                                                                                                                   8 C; 15 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cox WI;
                                                                                           .
                                                                                                                          Score 16.6;
Pred. No. 2e
                                                                                                 Mismatches
                                                                                                                          2e+02;
                                                                                                                                                       DB 2;
                                                                                              4.
                                                                                                                                                       Length 42;
                                                                                                 Indels
                                                                                           0;
                                                                                              Gaps
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SAX 5

AAH02411;

AAH02411 standard;

DNA;

100 ВÞ 밁 Ş

36 ω

GGCGCCAACCTGCTAGGGATTTT 25

GGGCGCCACCTGCTAGGGATTTT 57

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RESULT 10
ABK93894
ID 93893
XX ABK93
XX ABK93
XX 29-AU
DT 26-AU
XX Human
XX
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                                                                                                                                                                                         The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with contact and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide base sequence, and detecting the amplified NA; or providing a hybridisation probe and detectable label, hybridising HIV-2 NA with the probe to form probe target duplex, and detecting the duplex. The method is useful for detecting the presence of HIV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C and D of HIV-2. The method is useful for amplifying and detection to blood serum and also as components of multiplex amplification creations that synthesise amplicons corresponding to polynucleotides of unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the creation. (Updated on 29-AUG-2003 to standardise OS field)
       Matches
                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:tar;
                                                                                                                                 Sequence 57 BP; 17 A; 14 C; 14 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2003
26-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B hepatitis C virus; HCV; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 2 detection probe #18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK93894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-489953/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-2000; 2000US-0242620P.
30-MAR-2001; 2001US-0280058P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YY,
   19;
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                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burrell TA;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58pp; English.
                            66.4%;
82.6%;
   0,
                                   Score 16.6;
Pred. No. 2
       Mismatches
                                   .1e+02;
                                                                  DB 6;
                                                                  Length
       Indels
                                                                      57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe:target
Gaps
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XX PRAX SOX X PRAX SOX X PRAX X PRAX X SOX X
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AAH02412
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Best Local S
Matches 18
                                13-OCT-2000; 2000WO-US028413
                                                                                                                                                                                                    drug
                                                                                                                                                                                                                                                                 Human
                                                                              19-APR-2001.
                                                                                                                       WO200127857-A2
                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                   Database; polymorphism;
                                                                                                                                                                                                                                                                                                        12-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                              AAH02412 standard; DNA;
                                                                                                                                                                                                                                                                                                                                               AAH02412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a database of human samples obtained from healthy individuals which can be used to identify polymorphic genetic markers. Data obtained for the database can be used to sort the samples by parameters such as age, sex and ethnicity. This is useful in linking markers with diseases, susceptibility to infection and drug responses. The present sequence was used in an assay to demonstrate the uses of the database of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Page 303; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing a database for identifying polymorphic genetic n comprises obtaining data relating to members of a healthy entering the information into a database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Braun
Chiu P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUL-2000;
10-JUL-2000;
19-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-273865/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-OCT-2000; 2000WO-US028413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SEQU-)
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2000US-0217658P.
2000US-00663968.
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85.7%;
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Pred. No. 3.7e+02;
0; Mismatches 3;
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RESULT 13
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Best Local
                                                                                                   Example 4; Page 21; 35pp;
                                                                                                                                                                                                WPI; 2003-222536/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CN1380303-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; retinoblastoma binding protein 34.54; tumour; 8s; primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a database of human samples obtained from healthy individuals which can be used to identify polymorphic genetic markers. Data obtained for the database can be used to sort the samples by parameters such as age, sex and ethnicity. This is useful in linking markers with diseases, susceptibility to infection and drug responses. The present sequence was used in an assay to demonstrate the uses of the database of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 100 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing a database for identifying polymorphic genetic markers, comprises obtaining data relating to members of a healthy population and entering the information into a database.
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10-JUL-2000; 2000US-0217251P.
10-JUL-2000; 2000US-0217658P.
19-SEP-2000; 2000US-00663968.
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                                                                                                                                           polypeptide-human retinoblastoma
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                                                                                                                                                                                                                                                                                   SHANGHAI BIOWINDOW GENE
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18; Conservative
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Jurinke C;
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85.7%;
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Pred. No. 3.7e+02;
0; Mismatches 3
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The present invention relates to human retinoblastoma binding protein 34.54, used to treat various tumours. The present sequence represents primer related to human retinoblastoma binding protein encoding sequen

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RESULT 14
ABA05816/c
ID ABA058
XX ABA058
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RESULT 15
AAT68636/c
ID AAT686
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DT 14-AUG
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Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of human ubiquitin-like protein 14. The sequences can be used in the treatment of cancer, haemopathy and HIV infection. The present sequence is a probe for the coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ubiquitin-like protein 14; cancer; haemopathy; HIV infection; gene therapy; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 19 (Disclosure); 31pp; Chinese.
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  DNA integration; LexA; HIV-1; FIV; integrase;
                                                                           V1/T2 substrate for integration assay.
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                                                                                                                                                                                                                                 AAT68636 standard; DNA; 33 BP
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.6; DB 6; Length Pred. No. 6.3e+02; O; Mismatches 4; Indels
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Pred. No. 4.8e+02;
0; Mismatches 2
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Search completed: August 31, Job time: 166.935 secs
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Matches 19
                                                                                                                                                                                                                        A substrate for assaying the disintegration activity of novel integrase-lexA fusion proteins (see also AAW17781-84), the Y-Oligomer, is prept. by annealing labelled Oligonucleotide T1 (AAY68633) with Oligonucleotides T3 (AAY68634), V2 (AAY68635) and V1/T2 (AAY68636). The reaction is performed with 5 nM of the Y-Oligomer and 250 nM of protein. The 5' end-labelled T1 strand of the Y-Oligomer migrates as a 16-nucleotide on denaturing gel. The disintegration product is a 30-mer. Fusion protein IN1-288/LexA (AAW1782) showed over 150% of the disintegration activity of HIV-1
                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein comprising retroviral integrase and DNA binding regions useful for integrating donor DNA into specific sites on target DNA, especially for inactivating oncogene(s) or inserting therapeutic genes.
                                                                                                                                                                                  Sequence 33
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19; Conserv
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CLEN LIVE IS TOWN SILL.

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Result
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                                                                              TITLE
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Trichoderma reesei EST dataset
Unpublished (2003)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0020
Fax: 919-513-0024
Email: ralph dean@ncsu.edu
Seg primer: LT-F1 primer.
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14
                                                                                                          Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 62)
                                                                                                                                                                 62 bp mRNA linear EST 31-OCT-2003 tric082xk23.bl1 T.reesei mycelial culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tric082xk23, mRNA sequence.
CF885516
                                                                                            Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D.,
Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M.
                                                                                                                                                           CF885516.1 GI:38140198
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AC566995

CG712371

BE2380126

RE2380126

RE2380526

RE35956581

BE25956581

BE25956581

BE25956581

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CG781268

AG513131

AU106807

CG7127331

CG519780

CG712733

CG519780

CG7127446

BE908831
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AI014256
BUB16046
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AA491818
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BJ057939
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AA065383
AZ600786
CG199846
CC1002253
U44135
F33772
BM126072
AZ521677
CB201994
CB211074
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BJ907426 GJ063502
AA065383 m151e06.r
AZ600786 1M0418F15
CG3399846 0180423-0
CL002253 0280069-0
U44115 ENU44135 AB
F33772 HSPD27429 H
BM126072 1f05b10.x
AZ921627 10060300.x
AZ921628 SALK_1146
BR21348 SE5 Chromos
BR6884 Human exon
AJ547093 Dr0sophil
AZ8251 H.sapiens D
BZ595658 SALK_08940
CG781268 112304400
AA513131 nh78f09.s
AU106807 AU106807
CG712301 111902760
CG554070 OST167335
CG712601 111902730
CG554070 OST167335
CG512780 OST81933
AA778587 af86f10.s
CG619780 OST823557
AG217446 Drosophil
AI014256 am50d10.s
BU816046 NU59E07 P
BZ763567 SALK_1193
AT063110 AT06310
AA491818 ng16b12.s
CK108605 1044P93 P
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: M. Bento Soares, Ph.D.
CONA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 527 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 100)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GCGCCAACCTGCTAGGGATTTT 25
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           /clone_lib="NCI_CGAP_CO3"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site 2: Eco RI; lst strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo (dT) primer. Double-stranded cDNA was I spated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. "
                                                                                                                                                                                                                                                          "booled"
                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:880802"
                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                           tissue_type="colon"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
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/clone_lib="T.reesei mycelial culture, Version 6 October
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/clone="tric082xk23"
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/mol_type="mRNA"
/strain="QM6a"
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Pred. No. 1.1e+04;
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AI256079
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: custom primer used 
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality possible reversed clone: similarity o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 82)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Al256079 82 bp mRNA linear EST 12-NOV-1998 ui94912.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1890118 3' similar to SW:COX3_RAT P05505 CYTOCHROME C OXIDASE POTIVEREDTITE TIT . ""BNA "COXIDASE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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19; Conserva
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/clone_lib="Sugano mouse liver mlia"
/note="forgan: liver; Vector: pMRS18S-FL3; Site_1: DraIII
/note="forgan: liver; Vector: pMRS18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG]; digested
and cloned into distinct DraIII sites of the pMRS18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:1890118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                         dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                 lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                sex="female"
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76.0%;
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Pred. No. 1.6e+04;
D; Mismatches 6;
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Query Match Best Local Similarity

57.6%; 75.0%;

Score 14.4; DB 9; Pred. No. 4.2e+04;

Length 82;

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JOURNAL COMMENT
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AUTHORS
TITLE
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CB165114/c
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                    48
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CB165114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Perugia
Borgo XX giugno 74, 06121, Perugia, Italy
Tel: +390755856211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Rosellini, D.
Dipartimento di Biologia Vegetale e Biotecnologie Agroambientali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Medicago sativa
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Isolation of expressed sequence tags from developing female sterile and female fertile alfalfa plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB165114 92 bp mRNA linear EST 30-JAN-2003
44 Alfalfa developing flower bud library Medicago sativa cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago.
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                                                          GGGCGCCAACCTGCTAGGGATTTT 25
                      GGTAGTCAACCTTCTATAGATTTT
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                                                                                                 Conservative
                                                                                                                                                                                         /clone lib="Alfalfa developing flower bud library"
/clone lib="Alfalfa developing flower buds; Vector: Invitrogen
/clone "Organ: Developing flower buds; Vector: Invitrogen
PCR4 TOPO Vector; This EST was obtained with the cDNA-AFLP
method (Bachem et al.Plant Journal 9:745-753, 1996). Total
RNA was extracted from three female fertile and three
female sterile alfalfa plants from an P1 population
obtained by crossing the plants B17 and P13 (Rosellini et
al. Theoretical and Applied Genetics, 97:1 289- 1295,
1998). Equal amounts of RNA from each fertile or sterile
plant were bulked and used for the CDNA-AFLP protocol.
The restriction endonucleases EcoRI and MseI were used.
Bands that were polymorphic between the female sterile and
female fertile bulks were isolated from the polyacrilamide
gel, cloned in a plasmid vector (Invitrogen PCR4 TOPO) and
sequenced using the M13F primer. The published sequence
begins and ends with the EcoRI (GAATTC) and MseI (TTAA)
recognition sequences, respectively. The technical help of
Francesco Panara is gratefully acknowledged."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roselli@unipg.it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="hermaphrodite"
/dev_stage="From ovule primordia to anthesis"
/lab_host="B.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago sativa"
/mol_type="mRNA"
/cultivar="B17 x P13 F1 population"
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                                                                                                                Score 14.4; DB 14
Pred. No. 4.4e+04;
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                  25
                                                                                                                                     DB 14;
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LOCUS
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BJ057939
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RESULT

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AUTHORS
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Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                       BJ057939 NIBB Mochii normalized Xenopus tailbud library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Michael J. Brownstein, Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 62)
Kitayama,A.,
Kohara,Y.
                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 72)
                                                                                                                                       Xenopus laevis
                                                                                                                                                                                                                    BJ057939.1 GI:17492296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI669171.1 GI:4833945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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                                                                                                                                                                    Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                laevis cDNA clone XL103o03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCAACCTGCTAGGGATTT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCAAGCTGCAGGGGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="IMAGE:2312082"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lab_host="DH10B"
                 Terasaka, C., Mochii, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.8%;
84.2%;
                                                                                                                                                                 (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         38
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Pred. No. 4.8e+04;
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sapiens cDNA clone IMAGE:2312082 3',
                 Ueno, N., Shin-i, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Xenopus
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REFERENCE
AUTHORS
TITLE
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VERSION
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BI907426
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 41)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
Plate: LLAM11534 row: c column: 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI907426.1 GI:16170258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Nishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tshini@genes.nig.ac.jp
The information of this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://xenopus.nibb.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCCAACTINNIGGGGNTTTT 38
                                                                                                                                                                                                                                       quality sequence stop: 41.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nilarity 72.7%;
Conservative
                                                                                                          /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="MAGE:5212728"
/tissue_type="laukocyte"
/lab_host="DH10B"
/clone lib="NIH MGC 118"
/clone lib="NIH MGC 118"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL103003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.2; DB:
Pred. No. 5e+04;
0; Mismatches
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sapiens cDNA clone IMAGE:5212728 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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ORIGIN
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Matches 17
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SOURCE
ORGANISM
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AA065383/c
LOCUS
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Matches :
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                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                            Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 90.
Location/Qualifiers
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 96)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA065383 96 bp mRNA linear EST 03 mL51e06.r1 Stratagene mouse testis (#937308) Mus musculus clone IMAGE:515554 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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EST.
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17; Conserv
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          56.0%;
iilarity 77.3%;
Conservative (
                                                                                   Conservative
                                                                                                                                                                                                                                                sex="males"
                                                                                                                                                                                                                                                              clone="IMAGE:515554"
                                                                                                                                                                                                                                                                                db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                strain="CD-1"
                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cloning). Average insert size 1.7 kb, insert si 1.2-3.3 kb. Library is normalized and enriched full-length clones and was constructed by C. Gru (Invitrogen). Research Genetics tracking code 0 this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.0%;
77.3%;
     Score 14; DB 9; Length 96;
Pred. No. 6.7e+04;
0; Mismatches 5; Indels
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Pred. No. 5.2e+04;
лв »,
3.7e+04;
5;
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                                                                                                                   Primer:
XR Vector;
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de 027. Note:
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     Gaps
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3 GGCGCCAACCTGCTAGGGATTT

RESULT 9 AZ600786/c LOCUS

AZ600786

GSS 13-DEC-2000

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80

GGCGTCGACCTGCCCGGTATTT

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Best Local
                                                                       Matches
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                                                                       Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 10000 Std Error: (
Plate: 0418 row: F column: 15
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1M0418F15R Mouse 10kb plasmid clone UUGC1M0418F15 R, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
GGCGCCAACCTGCTAGGGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mmalia; Eutheria; (bases 1 to 97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 97.
Location/Qualifiers
                                                                       Conservative
                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi 4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mouse_10kb_plasmid_UUGC1M_library"
/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.
musculus_C57BL/6J_(male) was obtained_from_the_Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg.,
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="UUGC1M0418F15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ab_host="E. Coli strain XL10-Gold,
                                                                                           56.0%;
77.3%;
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                                                                                             Score 14;
Pred. No.
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                                                                         Mismatches
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mid UUGC1M library Mus musculus genomic
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                                                                                        DB 28;
6.8e+04;
                                                                       <u>ب</u>
                                                                                                                 Length 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the Jackson
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CG399846/c
LOCUS
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                                                                                                                                    ORGANISM
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                                                          Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                   02S0069-08C1-G08, genomic survey sequence.
CL002253
CL002253.1 GI:40219332
                                                                                                                                                                                                                                                                    CL002253 64 bp DNA linear GSS 19-02S0069-08C1-G08 UniformMu MuTAIL Library Zea mays genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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1 (bases 1 to 64)
Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                                                                                                                 GSS.
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University of Florida
PO 110690 Gainesville,
Tel: 352-392-1928 x322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 64)
Latshaw,S., Tan,B-.C., Sett
Sequence tagged transposon
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CG399846.1 GI:34398730
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: drm@ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                                                                                                                                                                                                                                                                            CGGTTGTCCAACTCCTAGCGATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4577"
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/clone lib="UniformMu MuTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
/niserrions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo assymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
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72.0%;
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MUTAIL Library Zea mays genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                            39
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JOURNAL COMMENT

Gaps

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Query Match
Best Local Similarity 72.09
                                                                                                                                                                                                                                Contact: Keon-Sang Chae
Chonbuk National University
Chonju, 561-756, S. Korea
                                                                                                                                                                                                                                                                                         Lee,D., Lee,S., Hwang,H., Kim,J. and Chae,K.
Quantitative analysis of gene expression in sexual structures of
Aspergillus nidulans by sequencing of 3'-directed cDNA clones
FEMS Microbiol. Lett. 138 (1), 71-76 (1996)
                                                                                                                                                                                                                                                                                                                                                        Emericella nidulans (anamorph: Aspergillus nidulans)
Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

1 (bases 1 to 73)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENU44135 Aspergillus midulans cle
cDNA clone SE0101, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              U44135.1 GI:1244798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGCGCCAACCTGCTAGGGATTTT 25
                                                                                                                                                                                                         +82-652-70-3345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence flanking probable Mu insertion site in UniformMu line: 0280069-08, Primer set; C
Class: transposon insertion site.
Location/Qualifiers
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PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-992-1928 x322
Email: drm@ufl.edu
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Unpublished (2003)
Contact: Donald R.
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Plant Molecular and Cellular Biology Program
                                                                                                                                                                    chaeks@chonbuknms.chonbuk.ac.kr.
Location/Qualifiers
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/clone="0250069-08C1-G08"
/clone="0250069-08C1-G08"
/clone="0250069-08C1-G08"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the interlaced PCR (TAIL) protocol using primers specific for primers. Amplicons were size enriched using sepharose 400 spin columns and cloned into the TOPO PCR4 vector."
                                                /tissue_type="cleistothecium"
/cell_type="Hull cell"
                                                                            /db_xref="taxon:162425"
/clone="SE0101"
                                                                                                            /organism="Emericella nidulans"
|mol type="mRNA"
|strain="FGSC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bzl-m9)"
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lane cleistothecium Emericella nidulans
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                   RESULT 14
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                                                                                                        w
                                                                                           GGCGCCAACCTGCTAGG 19
                                                                  GCCGCCAACCTCCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Valle G.
GRIBI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW
http://grup.bio.unipd.it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 75)

Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavi Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G. 3'-end-specific cDNA library of human skeletal muscle by DN Genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F33772
HSPD27429 HM3 Homo sapiens cDNA clone s3000010H07,
F33772.1 GI:4819398
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                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                       (tissue_type="pectoral muscle (after mastectomy)"
|clone_Tib="HM3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                sex="female"
                                                                                                                                      55.2%;
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/note="3'-directed cDNA clones; single-pass sequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.2%; Score 13.8; DB 14; 72.0%; Pred. No. 7.6e+04; tive 0; Mismatches 7;
                                                                    21
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                                                                                                                  Score 13.8; DB 14;
Pred. No. 7.7e+04;
0; Mismatches 2;
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Catarrhini; Hominidae; Homo.
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mRNA sequence.
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FEATURES

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JOURNAL MEDLINE PUBMED COMMENT

REFERENCE AUTHORS TITLE

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 12 U44135 LOCUS DEFINITION

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RESULT 15
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                                                   AZ921627 94 l
1006030G08.x2 1006 - RescueMu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing
Library was constructed by Dr. Douglas Melton DNA sequencing
Washington University Genome Sequencing Center For information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
survey sequence.
AZ921627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu) This sequence now available from the IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrine Pancreas Consortium 
Unpublished (2000)
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          consortium, for clone orders contact: info@image.llnl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
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                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORTL; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT prining. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Search completed: August 31, 2004, 03:09:39 Job time: 1269.56 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: walbot@stanford.edu
Plate: 1006030 row: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize genomic sequences found using engineered RescueMu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walbot, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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GSS.
                                                                                                        Similarity
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                                        CGGGCGCCAACCTGCTAGGGATTTT 25
CAGGCCCCGCCTCATTTGGATTTT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to
                                                                                  Conservative
                                                                                                                                                                                                            pBlueScript backbone); Site 1: BamHI; Site 2: BgIII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.rmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates wit
                                                                                                                                                                                            ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:4577"
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72.0%;
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                                                                                                          Score 13.8; DB 28
Pred. No. 8.3e+04;
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المستحدد لالملكيات عافيلام الالالتال

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
         GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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                      US-09-102-830-31
US-08-105-483-160
US-08-105-29-31
US-08-303-275-48
US-08-458-101-160
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US-08-458-101-160
US-08-458-101-160
US-09-552-950-22
US-09-393-171-2
US-09-442-806-13
US-08-442-806-13
US-08-442-806-13
US-08-4137-175A-18
US-08-4137-175A-18
US-08-414-430-12
US-08-414-430-12
US-08-414-430-12
US-08-418-682-22
US-08-418-682-22
US-08-481-682-22
US-08-481-682-22
US-08-481-682-23
US-08-481-682-23
US-08-481-682-23
US-08-481-68-23
US-08-481-848A-23
US-08-481-8848A-23
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Sequence 31, Appl Sequence 160, App Sequence 160, Appl Sequence 62, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 19, Appl Sequence 10, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 23, Appl Sequence 33, Appl Sequence 31, Appl Sequence 31, Appl Sequence 14, Appl Sequence 16, Appl Sequence 31, Appl Sequence 31
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Query Matc Best Local Matches	SULT 1 Sequence 31, Applica Patent No. 6001558 GENERAL INFORMATION APPLICANT: BACKU APPLICANT: CASEY APPLICANT: CASEY APPLICANT: COMMITTIE OF INVENTION TITLE OF INVENTION TORNET OF SEQUENCE COUNTRY: USA ZIP: 08933 COMPUTER READABLE MEDIUM TYPE: Pate SOFTWARE: Pate SOFTWARE: Pate CURRENT APPLICATION TILING DATE: CLASSIFICATION NUM FILING DATE: CLASSIFICATION NAME: OGDEN, S' REGISTRATION FOR SEQ SEQUENCE CHARACTEE LENGTH: 22 bas TYPE: nucleic TYPE: TOPOLOGY: 1ine MOLECULE TYPE: D 3-09-102-830-31	86012895	33 33 33 33 33 33 33
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68. 100 tive	ion US/0 , JOHN W , ANU E , ANU E SEN, ERI S, THOMA S, THOMA S, AMPLI E AND/O S: 34 SON & JO NSON & JO NS	97 20 33 78 78	96 38 38 78 78 84 84 97
. 0 % ;	OHN W SUSAN M N ERIC B THOMAS J AMPLIFICATION AND/OR HIV-2 34 SS: SCOMPACTIBLE PC-DOS/MS-DOS RELEASE #1.0 DATION: I US/09/102,8 I US/09/102,8 I US/09/102,8 I US/09/102,8 I US/09/102,8 I US/09/103,8		2444446000
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re 17; DB ed. No. 12 Mismatches	7/ 30 A	09-434-122 08-866-340 09-103-875 09-336-946 08-387-805 08-387-805 08-113-750 08-829-876 09-234-874	836- 836-
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TELEPHONE: (212) 840-0712

TELEPAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 16

SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs

TYPE: nucleic acid

TYPE: nucleic single
                                                                                                                     Sequence 160, Application US/08709209
PATENT NO. 5762938
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NIMMER OF GENETICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-08-105-483-160
                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: Paolet
STREET: 530
STREET: 530
CITY: New York
THE: NY
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
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TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
                                                         ADDRESSEE: C/o William S. Frommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 530 Fift
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Curtis, Morris & Safford
                                                                                                                                                                                                                                                                                                                                                            19;
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o. 5494807
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                                              530 Fifth Avenue
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82.6%;
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// Pred. No. 22;
0; Mismatches
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US-08-303-275-48
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILING DATE: 21-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Paolet
APPLICANT: Tarta;
APPLICANT: Cox, 1
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                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 11-UNN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                        APPLICATION NUMBER: FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
REGISTRATION NUMBER:
                                                                                                         CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer
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    Application US/08303275
    5766598

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                                                               US 07/897,382
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US-08-458-101-160
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                                                                TELEFAX: (212) 840-071
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                        ZIP: 10030
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/458,101
                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0:
FILING DATE: 01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue
            LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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 POPOLOGY:
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1 Similarity 82.6%;
19; Conservative
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Pincus, Steven E.
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linear
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iviere, Michel
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                                                                                                    840-0712
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Pred. No. 22;
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RESULT 7 US-09-758-282B-151

GENERAL Sequence 151,

INFORMATION:

APPLICANT: Ma, Wu-Po APPLICANT: Lyamichev

APPLICANT:

Lyamichev, Victor I.
Kaiser, Michael W.
Lyamicheva, Natalie E.
Allawi, Hatim T.

Schaefer, James J. Neri, Bruce P.

APPLICANT APPLICANT

Patent No. 663546

Application US/09758282E

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US-08-455-968E-62/c
                                                                                                                             US-08-455-968E-62
                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                Best Local Similarity
                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 62,
                                                                                                                                                                                                       TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,968E
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Harrington, John L.
APPLICANT: Heieh, Chih-Lin
APPLICANT: Libber, Michael
TITLE OF INVENTION: Mammalian Flap-Specific Endonuclease
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend and Crew LLP
                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                   LENGTH: 33 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                       CELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Conservative
   31
                                                              19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5874283
CGACCTGCAGCCTGCTAGAGATTTT
                                  CGGGCGCCAACCTGCTAGGGATTTT 25
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                                                                 Conservative
                                                                                                                                                           linear
                                                                                                                                                                                                                                                                          415-576-0200
                                                                                                                                            DNA (oligonucleotide)
                                                                                                                                                                          single
                                                                                61.6%;
76.0%;
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82.6%;
                                                                                                                                                                                                                                                                                                                 36,429
                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                        18985-000100
                                                                                Score 15.4;
Pred. No. 86;
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Pred. No. 22;
                                                                                              DB
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                                                                                             Length 33;
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                                                                 Gaps
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Gaps

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US-09-393-171-22
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                                                            NUMBER OF SEQ ID NOS: 25
SEQ ID NO 22
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-552-950-22
                                                                                                                                                                                                                                                                                  Sequence 22, Applicate Patent No. 6673569
GENERAL INFORMATION:
                                                                                                         APPLICANT: KUROKAWA, Yoichi
APPLICANT: YANAGI, Hideki
APPLICANT: YANAGI, Takashi
IITLE OF INVENTION: DabA/DabB/DsbC/DsbD expression plasmid
FILE REFERENCE: 1422-391P
CURRENT APPLICATION NUMBER: US/09/393,171
CURRENT FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: JP 10/255702
EARLIER FILING DATE: 1998-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.6%; Score 15.4; Best Local Similarity 76.0%; Pred. No. 88; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: US-09-758-282B-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/552,950
CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Oxford Biomedica (UK) Limited
TITLE OF INVENTION: Anti-Viral Vectors
FILE REFERENCE: 674524-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09552950 Patent No. 6541248
                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 61.6%; Score 15.4; Best Local Similarity 94.1%; Pred. No. 8 Matches 16; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Enzymes for the Detection of Nucleic Acid Sequences FILE REFERENCE: FORS 04931 CURRENT APPLICATION NUMBER: US/09/758,282B CURRENT FILING DATE: 2001-01-11 PRIOR APPLICATION NUMBER: 09/577,304 PRIOR FILING DATE: 2000-05-24 NUMBER OF SEQ ID NOS: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                12 CGGGCCCGCCACTGCTAGAGATTTT 36
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    Application US/09393171
6673569

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                       US-08-068-945A-13
        Query Match 56.8%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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US-08-068-945A-13/c
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                                                                                                                                                                                                                 TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-393-171-22
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMERS: SE 9201809-2
PRIOR APPLICATION UNMERS: SE 9201809-2
PRIOR APPLICATION DATA:
APPLICATION UNMERS: SE 9201826-6
PILING DATE: 12-JUN-1992
PRIOR APPLICATION UNMERS: SE 9202088-2
PRIOR APPLICATION UNMERS: SE 9202088-2
PRIOR APPLICATION DATA:
APPLICATION UNMERS: SE 9202088-2
PRIOR APPLICATION OBJATA:
APPLICATION UNMERS: SE 9202088-2
PRIOR APPLICATION DATA:
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Matches
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                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEPHONE: (212)819-8783
                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                      LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1155 Ave.
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tornell, Jan
TITLE OF INVENTION: New DNA Sequences
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08 FILING DATE: 27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States ZIP: 10036-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGCGCGAAACTGCTGGGTATTGT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGCGCCAACCTGCTAGGGATTTT 25
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bjursell, Gunnar
Carlsson, Peter
Enerback, Sven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lidberg, Ulf
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                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1993
                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                 SE 9300902-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jeanette
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75.0%;
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  0;
Score 14.2; DB 1;
Pred. No. 3.3e+02;
0; Mismatches 3;
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Pred. No. 3.2e+02;
0; Mismatches 6;
                                    Length 24;
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RESULT 11
US-08-442-806-13/c
                                                                                                       US-08-442-806-13
                                                                                                                                                   TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13,
Patent No. 5
                                 Matches
                                                 Best Local Similarity
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201809-2
FILLING DATE: 11-JUN-1992
PRIOR APPLICATION NUMBER: SE 9201826-6
FILLING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: SE 9202088-2
PRIOR APPLICATION NUMBER: SE 9202088-2
PRIOR APPLICATION NUMBER: SE 9300902-5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300902-5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300902-5
PRIOR APPLICATION NUMBER: SE 9300902-5
PRIOR APPLICATION NUMBER: SE 9300902-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION UDBER: US 08/068,945
FILING DATE: 27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,806
                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                  NAME: Sterner, Richard J
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States ZIP: 10036-2787
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                                 16; Conservative
3 GGCGCCAACCTGCTAGGGA 21
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1155 Avenue of the Americas
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Carlsson,
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Tornell, Jan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enerback,
                                                                                                                                                                                                                                                                (212) 819-8783
                                                                                                                      DNA (genomic)
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Ulf
                                                 56.8%;
84.2%;
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Encoding Hum
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                                                                                                                                                                                                                                                                                                           35,372
                                                                                                                                                                                                                               13:
                                 0; Mismatches
                                                   Score 14.2;
Pred. No. 3
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                                                   3.3e+02;
                                                                  DB 1;
                                                                Length 24;
                                 Indels
                                 0
                                 Gaps
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                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: 
; OTHER INFORMATION: oligonucleotide 
US-09-625-188-27
                                                                                                                                                                                                                                                                                                                                          US-09-625-188-27; Sequence 27; A
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US-08-748-068-14
                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-748-068-14
Query Match
Best Local Similarity 77...
Thes 17; Conservative
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/625,188
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO.27
LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIA Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,068
FILING DATE: 12-NOV-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
08/256,959
FILING DATE: 05-OCT-1994
APPLICATION NUMBER: 08/256,959
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 04702.6
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: No. 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                        LENGTH: 65
                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-MAR-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Ch
NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
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6307037
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GGCGCCAGCTGCGAGGGA 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 base pairs
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PB/5-31285P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.8%;
                                  56.0%;
77.3%;
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                   Score 14; DB
Pred. No. 5e+0
0; Mismatches
                      0
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Pred. No. 3.5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                    DB 4;
5e+02;
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                      5
                                                 Length 65;
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                      Indels
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                    Gaps
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CGGGCGCCAACCTGCTAGGGAT 22

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RESULT 15
US-08-479-017-18/c
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            Sequence 18, Application US/08479017
Patent NO. 6143872
GENERAL INFORMATION:
APPLICANT: BARBOUR, Alan G.
APPLICANT: BERGSTROEM, Sven
APPLICANT: HANGSON, Lennart
TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
TITLE OF INVENTION: PROPHYLAXIS
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.2%; Score 13.8; DB 1; Length 38; Best Local Similarity 88.2%; Pred. No. 5.7e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNUMBER: US/08/137,175A
FILING DATE: 26-OCT-1993
CLASSIFICATION UNUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
AFFICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: BARBOUR=1B
TELECOMMUNICATION INGORRANTION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF BEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BARBOUR, Alan G.
APPLICANT: BERGSTROEM, Sven
APPLICANT: HANSSON, Lennart
TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
TITLE OF INVENTION: PROPHYLAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 419 Sevent
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                20 CAACCTGCTAGCGAATT
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Search completed: August 31, 2004, 04:43:17 Job time : 40.2857 secs
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INFORMATION FOR SEQ ID NO: 16 SEQUENCE CHARACTERISTICS: LENGTH: 38 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/137,175
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVer P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BARBOUR=18
TELECOMMUNICATION INFORMATION:
TELEPAX: 202-638-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,017
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
                                                                                   20 CAACCTGCTAGCGAATT
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                                                                                                                                                                                                                                                                          linear
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Minimum DB seq length: 0
Maximum DB seq length: 100
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
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                Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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Gapop 10.0 , Gapext 1.0
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25
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PUBCOMB.seq:*
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SUMMARIES

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25 16.6 16.6 16.2 16.2 16.2 16.2 16.2	25 25	Score
100.0 72.0 66.4 64.8 64.8 64.8 64.8	100.0	Match Length
52 58 58 24 27 100 100 100 100 100	34 34	Length
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US-10-001-407-15 US-10-001-407-19 US-10-001-407-13 US-10-001-407-18 US-10-001-407-18 US-10-272-665-109 US-10-273-321-108 US-10-273-321-109 US-10-272-756-109 US-10-272-756-109	US-10-001-407-10 US-10-001-407-8 US-10-001-407-9	ID
Sequence 15, Appl Sequence 14, Appl Sequence 19, Appl Sequence 13, Appl Sequence 18, Appl Sequence 108, App Sequence 109, App Sequence 109, App Sequence 109, App Sequence 109, App Sequence 109, App Sequence 109, App	Sequence 10, Appl Sequence 8, Appli Sequence 9, Appli	Description

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75 75 75 75 75	667777	9998666993333 90066666	100 100 33 33
15 15 17 17	10 10 15 17 17	15 15 15 15 15 15 15 15 15 15 15 15 15 1	16 10 11
US-09-931-325A-98 US-09-930-915A-139 US-10-082-014-254 US-10-372-076-284 US-10-806-006-139 US-10-677-074-284 US-10-677-074-284 US-10-805-913-139			US-10-273-228-108 US-10-273-228-109 US-09-864-636A-292 US-09-758-282-151 US-09-864-426A-292
sequence 98, App Sequence 139, App Sequence 254, App Sequence 284, App Sequence 139, App Sequence 284, App Sequence 139, App	e 2855, e 2855	e 2927 21, AI e 22, I e 12, I e 23, I e 23, I e 24, I e 24, I e 24, I	Sequence 108, App Sequence 109, App Sequence 292, App Sequence 151, App Sequence 292, App

ALIGNMENTS

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US-10-01-407-10

US-10-01-407-10

is Sequence 10, Application US/10001407

publication No. US20020177127A1

GENERAL INFORMATION:

APPLICANT: Yang, Yeasing
APPLICANT: Burrel, Terrie

iTITLE OF INVENTION: Compositions and Methods for Detecting
iTITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)

FILE REPRENCE: GP117-03.UT

CURRENT FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: US/10/001,407

CURRENT APPLICATION NUMBER: US/280,058

PRIOR APPLICATION NUMBER: G0/242,620

PRIOR APPLICATION NUMBER: G0/240,620

PRIOR FILING DATE: 2001-03-30

INVEST OF SEQ ID NOS: 34

SOFTMARE: FastSEQ for Windows Version 3.0

LENGTH: 25

TYPE: DNA

GORGANISM: HIV-2

US-10-001-407-10

Query Match

Cuery Match

Cuery Match

100.0%; Scove 25; DB 14; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.0091;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

MUMBER OF SEQ ID NO: 0;

PRIOR FILING DATE: 2001-03-09;

ONGANISM: HIV-2

US-10-001-407-8/c

Sequence 8, Application US/10001407

Publication No. US20020177127A1
```

GENERAL INFORMATION

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US-10-001-407-15

Sequence 15, Application US/10001407

Publication No. US20020177127A1

GENERAL INFORMATION:

APPLICANT: Yang, Yeasing

APPLICANT: Burrell, Terrie

TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)

FILE REFERENCE: GP117-03.UT

CURRENT APPLICATION NUMBER: US/10/001,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yang, Yeasing
APPLICANT: Burrel, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03 UT
CURRENT APPLICATION NUMBER: US/10/001,407
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-32
PRIOR FILING DATE: 2000-10-32
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR PILING DATE: 2001-03-30
NUMBER OF SEO ID NOS: 34
SOFTWARE: FastSEO for Windows Version 3.0
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; ORGANISM: HIV-2
US-10-001-407-9
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APPLICANT: Yang, Yeasing
APPLICANT: Burrell, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03.UT
CURRENT APPLICATION NUMBER: US/10/001,407
FOURTH FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR APPLICATION NUMBER: 60/240,058
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 34
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; ORGANISM: HIV-2
US-10-001-407-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Publication No. US20020177127A1
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Best Local
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Sequence 14, Application US/10001407

Publication No. US20020177127A1

GENERAL INFORMATION:
APPLICANT: Yang, Yeasing
APPLICANT: Burrell, Terrie

TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)

FILE REFERENCE: GP117-03.UT

CURRENT APPLICATION NUMBER: US/10/001,407

PRIOR APPLICATION NUMBER: 60/242,620

PRIOR FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: 60/242,620

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/280,058

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 34

SOPTWARE: FastSEQ for Windows Version 3.0

LENGTH: 25

Type: DNA
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; ORGANISM: HIV-2
US-10-001-407-14
                                                                                                                                                                                                                Sequence 19, Application US/10001407 Publication No. US20020177127A1 GENERAL INFORMATION:
APPLICANT: Yang, Yeasing
APPLICANT: Burrell, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03 UT
CURRENT APPLICATION NUMBER: US/10/001,407
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
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US-10-001-407-14
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Best Local Similarity
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SEQ ID NO 15

ERNOTH: 52

TYPE: DNA

ORGANISM: Artificial Sequence

FRATURE:

OTHER INFORMATION: T7 promoter primer having a promoter sequence

OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary

OTHER INFORMATION: primer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 34
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SEQ ID NO 19
LENGTH: 58
TYPE: DNA
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: one nucleotide
US-10-001-407-13
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Best Local :
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LENGTH: 24
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      Matches
       APPLICANT: Yang, Yeasing
APPLICANT: Burrell, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03.UT
CURRENT APPLICATION NUMBER: US/10/001,407
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
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APPLICANT: Burrell, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03.UT
CURRENT APPLICATION NUMBER: US/10/001,407
CURRENT FILING DATE: 2001-10-22
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PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version
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SOFTWARE: FastSEQ for Windows Version
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PRIOR FILING DATE: 2001-03-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
41 CGGGCGCCAACCTGCTAG 58
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82.6%;
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Pred. No.
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Pred. No. 1
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Query Match
Best Local Similarity
Thes 19; Conserve
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US-10-272-665-109
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PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
Publication No. US20030180748A1
GENERAL INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING TITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-2031E
CURRENT APPLICATION UMMBER: US/10/272,665
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 57
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LENGTH: 100
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                                                                                                                                                                 Sequence 109,
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TITLE OF INVENTION: METHODS FOR GENERATING
TITLE OF INVENTION: GENETIC MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-03-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/687,483 PRIOR FILING DATE: 2000-07-10
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CURRENT FILING DATE: 2002-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 24736-2033E
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Hom sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: T7 promoter primer having a promoter sequence OTHER INFORMATION: appended at the 5' end of the sequence given as OTHER INFORMATION: SEQ ID NO:13
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                                                                                                                                                                                                                                                        64
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                                                                                                                                                                                                                                                                                          GGGCGCCAACCTGCTAGGGAT 22
                                                                                                                                                                                                                                                        GGGCGTCAACCTGCAAGGTAT
                                                                                                                                                 Application US/10272665 o. US20030180748A1
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o. US20030180748A1
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Pred. No. 1.9e
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Pred. No. 3.
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PRIOR APPLICATION NUMBER: 09/607,483
PRIOR APPLICATION NUMBER: 09/607,483
PRIOR APPLICATION NUMBER: 09/607,483
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR PILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR PILING DATE: 2000-09-19
NUMBER OF SEO ID NOS: 118
SOFTWARE: FREESEQ for Windows Version 4.0
PRIOR D 10 108
RESULT 12
US-10-273-321-109
; Sequence 109, Application US/10273321
; Sequence 109, Application US/10273321
; Publication No. US20030180749A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: GENETIC MARKERS
; TITLE OF INVENTION: GENETIC MARKERS
; FILE REFERENCE: 24736-2033B
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Matches
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; ORGANISM: Homo sapien
US-10-272-665-109
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-10-273-321-108
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PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
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Publication No. US20
GENERAL INFORMATION:
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Best Local :
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LENGTH: 100
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CURRENT FILING DATE: 2002-10-15
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APPLICATION NUMBER: 60/217,658
FILING DATE: 2000-07-10
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o. US20030180749A1
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ilarity 85.7%;
Conservative
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85.7%;
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Pred. No. 3.1e+02;
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Pred. No. 3.1e+02;
0; Mismatches 3
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US-10-272-756-109
      Sequence 109, Application US/10272756
Publication No. US20030190644A1
GENERAL INFORMATION:
APPLICANT: Braun et al.
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; TYPE: DNA
; ORGANISM: Homo s
US-10-273-321-109
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; TYPE: DNA
; ORGANISM: Hom sapien
US-10-272-756-108
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US-10-272-756-108
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Best Local
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FILE REFERENCE: 24736-2033C
CURRENT APPLICATION NUMBER: US/10/272,756
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/17,251
PRIOR APPLICATION NUMBER: 60/17,251
PRIOR APPLICATION NUMBER: 60/17,251
PRIOR APPLICATION NUMBER: 00/663,968
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 00/663,968
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
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APPLICANT: Braun et al.
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
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64 GGGCGTCAACCTGCAAGGTAT 84
                                     2 GGGCGCCAACCTGCTAGGGAT 22
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85.7%; Pred. No. 3.1¢
ative 0; Mismatches
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85.7%; Pred. No. 3.1¢
tive 0; Mismatches
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; SOFTWARE: FastSEQ for Wi
; SEQ ID NO 109
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-272-756-109
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Search completed: August 31, 2004, 06:17:02 Job time: 1823.08 secs
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US-10-273-228-108
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; TYPE: DNA
; ORGANISM: Hom sapien
US-10-273-228-108
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CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILLING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILLING DATE: 2000-07-10
PRIOR PRILING DATE: 2000-07-10
PRIOR FILLING DATE: 1999-10-13
PRIOR FILLING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILLING DATE: 2000-07-10
PRIOR FILLING DATE: 2000-07-10
PRIOR FILLING DATE: 2000-07-10
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PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-09-19
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Best Local Similarity 85.7
Matches 18; Conservative
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Best Local Similarity
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SEQ ID NO 108
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TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POTITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-2033D
CURRENT APPLICATION NUMBER: US/10/273,228
CURRENT FILING DATE: 2002-10-15
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PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FASTSEQ for Windows Version 4.0
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85.7%; Pred. No. 3.1e+02;
ative 0; Mismatches 3;
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Maximum Match
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Maximum DB
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS RESULT 1 AX498427 LOCUS DEFINITION ACCESSION VERSION Result No. SOURCE KEYWORDS a TITLE JOURNAL Score 36.4 36.4 36.4 Sequence AX498427 2 (hiv-2) Patent: WO 0234951-A 15 02-MAY-2002; Compositions and methods 2 (hiv-2) synthetic construct synthetic construct AX498427.1 GI:23343305 Yang,Y.Y. and Burrell,T.A. AX498427 artificial sequences Query 15 Length from \$\text{\$\tinteta}}\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\tex{ Patent 贸 XX498427 AXA074095 AXA074095 AXA98429 AXA98429 AXA074113 B61328 AX3344818 AX39773 B1023693 AX39773 B103693 AX397771 AR3452027 AR3452027 AR3452027 AR344848 AX397771 AR3452027 AR352027 AR3913285 AR34721018 AR34721018 AR34721018 AR352051 AR352051 AR352051 AR3602772 AR39530 AR3602772 AR39531 AR3602772 AR360272 AR360272 AR360272 AR360 I40641 I40642 I40643 52 bp WO0234951. ALIGNMENTS for detecting human immunodeficiency virus DNA linear AR352051 Sequence AX721018 Sequence AX802772 Sequence AX803190 Sequence AX400952 Sequence AX4074111 Sequence AR400956 Sequence AR400956 Sequence AR401956 Sequence AR401956 Sequence AR401956 Sequence AR401956 Sequence AR307449 Sequence AX025599 Sequence 9 BD080307 Nucleic a E61341 Probe for d AR352027 Sequence AR344816 Sequence AX397771 Sequence AX397771 Sequence AX397780 Sequence AX397803 Sequence AX210629 Sequence AX210629 Sequence AX210629 Sequence AX210629 Sequence AX210629 Sequence AX39128 Sequence AX39128 Sequence AX19128 Sequence AX19128 Sequence BD243351 Protectio 125930 Sequence BD13285 Methods o AX708731 Sequence E61325 Probe for d AR352051 Sequence AR400954 Sequence AX074113 Sequence E61328 Probe for d AR352014 Sequence AR344818 Sequence AX397773 Sequence AX39773 Sequence AX498427 Sequence AR400936 Sequence AX074095 Sequence AX498429 Sequence I40641 I40642 Description PAT 26-SEP-2002 Sequence 13 Sequence 14 Sequence 15

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Sequence 8 from Patent WO0104361.
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Bee,G.G., Yang,Y.Y., Kolk,D., Giachetti,C. and McDonough,S.
Detection of HIV-1 by nucleic acid amplification
Patent: US 6623920-A 8 23-SEP-2003;
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sequence, for HIV-1 LTR region"
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appended at the 5' end of an HIV-2
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1 (bases 1 to 51)

Bee,G.G., Yang,Y.Y., Kolk,D., Giachetti,C. and McDetection of HIV-1 by nucleic acid amplification Patent: US 6623920-A 26 23-SEP-2003;

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be Incorporated (US)
Location/Qualifiers
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OS ARTÍFICIAL Sequence
PN JP 199946778-A/2
PD 23-FEB-199
PF 14-JAN-1998 JP 199800
PR 11-JUL-1989 US
PI DANIEL LOUIS KASHIAN,
PC C12N15/09,C12Q1/68,C1
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1 (bases 1 to 54)

Daniel, L.K. and Timothy, J.F.

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11-JUL-1999 US 379501
DANIEL LOUIS KASHIAN,TIMOTHY
C12N15/09,C12Q1/68,C12N15/00
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   Conservative
                                                                                                                               /organism='Artificial
                                                                       /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="synthetic construct"
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/db xref="taxon:35830"
/noTe="synthetic amplification oligomer with
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Pred. No. 0.0016;
0; Mismatches 1;
Score 36; DB 6; Le
Pred. No. 0.0023;
0; Mismatches 10;
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AX397773
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AR344818
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Sequence
AR352014
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Patent: US 6582920-A 7, 24-JUN-2003;
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synthetic construct
                       AX397773.1
                                                                                                                                                       h 61.2%;
Similarity 76.5%;
39; Conservative
                                                                                                                                                                                                                                                                                                                                         Unknown
                                                                                                                                                                                                                                                                                                                                                                AR344818.1
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Location/Qualifiers
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Kacian,D.L., Fultz,T.J. and McDonough,S.H.
Detection of HIV
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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from Patent WO0220852
                       GI:21260647
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Pred. No. 0.0023;
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6589734.
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             AR307449
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                                                                                                                                                                                                                                                                                                                                         artificial sequences.

1 (bases 1 to 49)

Harvey, R.C. and Jr, T.J.C.

Nucleic acid sequence for detecting genetic biological samples
Patent: JP 2002535014-A 38 22-OCT-2002;
                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic construct synthetic construct
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JP 2002535014-A/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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Nucleic acid sequence for
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                                                                        AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTG 41
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Patent: WO 0220852-A 7 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US); Biomerieux S.A. (FR)
                                                            AAATTAATACGACTCACTATAGGGAGACTGTGGCTGACCTG
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JP 2002535014-A/38
22-OCT-2002
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28-JAN-1999 US 60/117640
RICHARD C HARVEY-HOWAS J CLLARK JR
C12N15/09,C12Q1/68,C12N15/00
Description of Artificial Sequence: synthetic construct promoter Location/Qualifiers
promoter (1) ...(28).
                                                                                                            Conservative
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ilarity 76.5%;
Conservative
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/mol_type="genomic DNA"
/db_xref="taxon;32630"
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer for Protease
sequence"
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for cancer in
     PAT 12-JUN-2003
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47 bp
Sequence 9 from Patent WO9907898
A99135
A99135.1 GI:6782088
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Detection of mycobacterium avium subspecies
Patent: WO 0034517-A 78 15-JUN-2000;
GEZONDHEIDSDIENST VOOR DIEREN (NL); MAANEN CORNELIS VAN (NL);
GEZONDHEIDSDIENST VOOR DIEREN (NL); MAANEN CORNELIS VAN (NL);
MACROSCREEN B V (NL); WAGTER LUCAS HENDRIK ALBERT (NL);
MICROSCREEN B V (NL); SCHUT FREDERIK (NL); BRINKHOF JOHANNES
MICRISCA MANTH (NL); ENSING HENRIETTE ZWAANTINA (NL); KOOPMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic construct synthetic construct
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AX025599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harvey, R. C. and Clark, T.J. Jr.
Nucleic acid sequences for detecting
a biological sample
Patent: US 6551778-A 38 22-APR-2003;
Location/Qualifiers
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AR307449
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ilarity 85.4%;
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/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
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/mol_type="genomic
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from Patent WO0034517.
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Pred. No. 0.16;
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ACCESSION
VERSION
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AUTHORS
TITLE
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AUTHORS
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Search completed: August 31, 2004, 02:04:25
Job time : 1096.38 secs
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Matches 33
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                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                    artificial Sequences.

CE 1 (bases 1 to 47)

CE 2010smit,J., Oudshoorn,P., Jurriaans,S. and Lukashov,V.V.

RS Goudsmit,J., Oudshoorn,P., Jurriaans,S. and probes for amplifying and detecting all HIV-1 subtypes

and detecting all HIV-1 subtypes

PAUG-192 all HIV-1 subtypes

ARZO, NOBEL NV

OS Artificial Sequence

PA 2001512701-A/9

PD 28-AUG-2001

PF 05-AUG-1998 JP 2000506380

PF 05-AUG-1998 JP 2000506380

PF 05-AUG-1998 JP 2000506380

PF 08-AUG-1998 JP 2702455.8

PI JAAP GOUDSMIT,PIETER OUDSHOORN,SUZANNE JURRIAANS, PI

VLADIMIR VLADIMIROVICH LUKASHOV

PC C1201/68,C12N15/09,C12N15/00

CC Description of Artificial Sequence: synthetic oligonucleotide

FH Key

T Source / Organism='Artificial Sequence'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unclassified.

1 (bases 1 to 47)

1 (bases 5 to 47)

JURRIAANS, S. and Goudsmit, J.

NUCLEIC ACID SEQUENCES THAT CAN BE USED AS PRIMERS AND PROBES IN
THE AMPLIFICATION AND DETECTION OF ALL SUBTYPES OF HIV-1
PATENT: WO 9907889-A 9 18-FEB-1999;

JURRIAANS SUZANNE (NL); AKZO NOBEL NV (NL)

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
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                                                                                  N
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                                                                                                                                                                33; Conservative
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A7 bp DNA linear PAT 27-AUG-2002 Nucleic acid sequences usable as primers and probes for amplifying and detecting all HIV-1 subtypes.
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Location/Qualifiers
1. .47
                                                                                                                                                                                                                                                                /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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                                                                                                                                                            60.0%; Score 31.2; DB 6; 91.7%; Pred. No. 0.19; tive 0; Mismatches 3;
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1: geneseqn1980s:*
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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
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Match
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52
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AAF56558
AAV66330
AAQ86607
AAT15552
AAX23172
AAD62557
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AAF56540
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Abk93891 Human imm
Aaf56540 HIV-1 det
Abk93893 Human imm
Aaf56558 HIV-1 det
Aav66330 Human imm
Aag86607 Human imm
Aat15552 Human imm
Aat15552 Human imm
Aat23172 HIV regio
Aad62557 Human imm
Abk53107 HIV-1 pro
Aaa63315 Mycobacte
Aaa76206 Human pro
Aaa63315 Mycobacte
Aax26214 Oligo com
Ade48105 Primer #1
Aaq56491 PCR prime
Aat91790 Primer BB
Aag86630 Modified
Aat15575 Multiple
Aat15575 Multiple
Aat15565 Human imm
Aat42408 HIV probe
Aat42408 HIV probe
Aat42408 HIV probe
Aat43408 HIV probe
                                                                                                                                                                                                                                                                            Description
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AAA76206 AAA63315 AAX26214 AAX26219 AAQ56491 AAQ56491790 AAQ86630 AAQ86630 AAQ86630 AAT15575

The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with 1st and 2nd amplification oligonucleotides, amplifying HTV-2 nucleotide base sequence, and detecting the amplified NA; or providing a hybridisation probe and detectable label, hybridising HTV-2 NA with the probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the presence of HTV-2 NAs in a lysate or a blood product such as plasma or serum, and also for detecting subtypes A, B, C

Detecting human immunodeficiency virus-2 nucleic acids in a sample, by amplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:target

Claim 11; Page 25; 58pp; English.

duplex.

WPI; 2002-489953/52.

31.8 31.4 31.4 31.2

ABK53107 AAL45469

30.4

4	44	43	42	41	40	39	38	37	36	35	<u>ب</u>	y y	32	31	30	29	28	27	26	25	24
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56.2	56.5	56.5	•	56.9	56.9	56.9	56.9	57.3	57.3	57.3	57.3	57.3	57.3	58.1	58.1	58.1	58.1	œ	58.5	8	58.5
45	51	47	52	47	47	47	47	4. 89	48	48	48	48	4.8	53	53	50	50	52	52	52	52
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AA086640	ABT12953	AAT91784	ACC43281	AAA89903	AAX57024	AAQ57043	AAQ50478	ABS57299	AAC93118	AAC97508	AAA77716	AAC58539	AAZ23689	AAL45499	ABK53137	AAL45467	ABK53105	AAD62570	AAX23185	AAX23208	AAV66357
Aag86640	Abt12953	Aat91784	Acc43281	Aaa89903	Aax57024	Aaq57043	Aaq50478	Abs57299	Aac93118	Aac97508	Aaa77716	Aac58539	Aaz23689	Aa145499	Abk53137	Aal45467	Abk53105	Aad62570	Aax23185	Aax23208	Aav66357
) Promoter	Mycobacte	Primer BB	•	_		M. tubero		Primer p1	Human PRO	Human PRO	Human PRO	Human DNA	Human pri	HIV-1 pol	HIV-1	HIV-1	6 HIV-1 Gag) Human imm	AIH	3 CML t (14;	OME-

ALIGNMENTS

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RESULT 1
ABK93891
Yang
                                                                                                                                                                                                                                                                  ABK93891;
                                                                                                                                         23-OCT-2000; 2000US-0242620P.
30-MAR-2001; 2001US-0280058P.
                                                                                                                                                            22-OCT-2001;
                                                                                                                                                                                                   Human immunodeficiency virus 2.
                                                                                                                                                                                                                                              29-AUG-2003
26-AUG-2002
                                                                                                                                                                          02-MAY-2002.
                                                                                                                                                                                      WO200234951-A2
                                                                                                                                                                                                              Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV; hepatitis C virus; HCV; probe; ss.
                                                                                                                                                                                                                                  Human immunodeficiency virus type 2 detection probe
                                                                                                                                                                                                                                                                               ABK93891
                                                                                                                             (GENP-) GEN-PROBE INC
                                                                                                                ΥΥ,
                                                                                                                                                                                                                                                                               standard;
                                                                                                                Burrell TA;
                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                             2001WO-US045396
                                                                                                                                                                                                                                                                               DNA;
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and D of HIV-2. The method is useful for amplifying and detecting the NI in blood serum and also as components of multiplex amplification reactions that synthesise amplicons corresponding to polynucleotides of unrelated viruses, e.g. HIV-1, hepatitis B virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the invention. (Updated on 29-AUG-2003 to standardise OS field)

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1 AATTTAATACGACTCACTATAGGGAGACGGGCGCAACCTGCTAGGGATTTT

Query Match Best Local S Matches 52

Similarity

100.0%; ilarity 100.0%; Conservative

Score 52; DB 6; Pred. No. 1.5e-12; Mismatches

Length 52

Indels

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Gaps

0

52

0

Sequence

52 BP; 15

A; 11 C;

13 G; 13 T; 0 U; 0 Other;

N

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Query Match
Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
AAF56540
                                                                                          The present invention provides probes and PCR primers for use in the detection of HIV-1. These are shown in AAF56533-AAF56589. They can used to diagnose HIV infection and to ensure that blood and blood products do not contain the virus, thus enabling the prevention of infection during blood transfusions. (Updated on 11-SEP-2003 to standardise OS field)
                                                                       Sequence 50 BP; 15 A; 10 C; 12 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                   Detecting HIV-1 nucleic acids in biological samples useful for diagnosing HIV-1 infection involves using nucleic acid capture oligomers, amplification oligomers and probe oligomers.
                                                                                                                                                                     Claim 5; Page 50; 60pp; English.
                                                                                                                                                                                                                                                             Bee
                                                                                                                                                                                                                                                                                                               (BEEG/)
                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000WO-US018685.
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18-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                    WO200104361-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                      immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection;
                                                                                                                                                                                                                                                                             ) GEN-PROBE INC.
) BEE G G.
) YANG Y Y.
) KOLK D P.
) GIACHETTI C.
) MCDONOUGH S H.
                                                Similarity
AATTTAATACGACTCACTATAGGGAGACGGGCCCAACCTGCTAGGGATTTT
                                                                                                                                                                                                                                                          Yang YY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTTAATACGACTCACTATAGGGGAGACGGGCGAACCTGCTAGGGATTTT
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first ent
                                                                                                                                                                                                                                                                                                                                                     99US-0143072P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; blood screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer SEQ ID NO:
                                                                                                                                                                                                                                                         Kolk DP,
                                             70.0%;
94.2%;
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                                Score 36.4; DE
Pred. No. 8.6e.
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                             3.6e-06;
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RESULT 4
AAF56558
ID AAF5
XX
AC AAF5
XX

standard;

DNA;

51

В₽

AAF56558; AAF56558 밁 Ś

1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTT

AATTTAATACGACTCACTATAGGGAGACGGGGGCGA--CTGCTAGAGATTTT

50 52 Matches Query Match Best Local :

Similarity

70.0%; 94.2%;

Conservative

0,

Pred. No. 8.66 0; Mismatches Score 36.4; Pred. No. 8.

.6e-06; BB 6

Length

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Gaps

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RESULT 3
ABK93893
AID ABK9
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                                             The invention relates to a method of detecting human immunodeficiency virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with 2C last and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide to base sequence, and detecting the amplified NA, or providing a CC probe to form probe and detectable label, hybridisally HIV-2. NA with the CC probe to form probe:target duplex, and detecting the duplex. The method is useful for detecting the presence of HIV-2. NAs in a lysate or a blood CC product such as plasma or serum, and also for detecting subtypes A, B, C CC and D of HIV-2. The method is useful for amplifying and detecting the NA CC reactions that synthesise amplicons corresponding to polynucleotides of CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C CC virus (HCV). ABK93977-ABK93910 represent HIV-2 detection probes of the vv
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                        Sequence 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting human immunodeficiency virus-2 nucleic acids in a sample, lamplifying nucleic acids with oligonucleotides and detecting nucleic acid, or hybridizing nucleic acid with a probe and detecting probe:t/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-2000; 2000US-0242620P.
30-MAR-2001; 2001US-0280058P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 2 detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B hepatitis C virus; HCV; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2003
26-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burrell TA;
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             BP; 15 A; 10 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; 58pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
12 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΒP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe:target
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides probes and PCR primers for use in the detection of HIV-1. These are shown in AAF56533-AAF56589. They can be used to diagnose HIV infection and to ensure the blood and blood products do not contain the virus, thus enabling the prevention of HIV infection during blood transfusions. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting HIV-1 nucleic acids in biological samples useful for diagnosing HIV-1 infection involves using nucleic acid capture oligomers, amplification oligomers and probe oligomers.
                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                 06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 51 BP; 15 A; 11 C; 12 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 54; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-147200/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (YANG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-2003
18-APR-2001
  06-JUN-1995;
                                                                                                                                                                                                                                                                                             Human immunodeficiency virus region 1 (+)
                                                                                                                                                                                                                                                                                                                                                                                                 AAV66330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV66330 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bee GG,
                                                20-OCT-1998.
                                                                                                                                                  Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; diagnosis; blood screening; PCR primer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection PCR primer SEQ ID
                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YANG Y Y.
KOLK D P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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MCDONOUGH S H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEN-PROBE INC.
BEE G G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang YY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTTAATACGACTCACTATAGGGAGACGGGCGCCA--CTGCTAGAGATTTT 50
                                                                                                                                                                                                                                               block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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(first entry)
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  95US-00469067.
                                                                                                                                                                                                                                               splice template;
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                                                                                                                                                                                                                                                                                                                                              entry)
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94.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36.4;
Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                 autocatalytic RNA amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĕ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                 primer;
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RESULT 6
AAQ8667
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XX AAQ8
XX AAQ8
DT 25-M
DT 15-N
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XX Prim
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XX Prim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV66330-31 represent Human immunodeficiency virus region 1 primers. The primers are used to exemplify the invention, together with probe AAV66332. The specification describes methods of synthesising multiple copies of a target nucleic acid sequence autocatalytically under conditions of substantially constant temparature, ionic strength and pH are provided in which multiple RNA copies of the target sequence autocatalytically generate additional copies. The target sequence is a block splice template which comprises two nucleic acid regions. The first region is located 3' of the second region and is blocked at its 3' terminus to inhibit primer extension by a DNA polymerase, and the second region comprises a promoter sequence recognised by an RNA polymerase. The methods are used for amplify nucleic acide agencially bun for arealwais.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 53 BP; 15 A; 11 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Block splice template useful for amplification of nucleic acids - comprises two nucleic acid regions, the first region located 3' of the second region and blocked at its 3' terminus to inhibit primer extension
                                                        WPI; 1995-130686/17.
                                                                                                                                                                                                                                11-JUL-1989;
10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methods are used to amplify nucleic acids, especially RNA,
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10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                          21-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer; autocatalytic; target; HIV;
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                                                                                                                                                                                                                                                                                                                 19-MAR-1992;
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                                                                                                                                                                          (GENP-) GEN-PROBE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTTAATACGACTCACTATAGGGAGAGACAAGGGACTTTCCGGCTGGGGACTTT
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                                                                                                           Kacian DL;
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(first entry)
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90US-00550837.
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90US-00550837.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; UB 2,
pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HIV) region 1 plus strand primer.
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Amplification of nucleic acid targets - using

a reverse transcriptase

EXEXOCOCOCXXX

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RESULT 7
AAT15552
ID AAT1
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Best Local S
Matches 42
The present sequence is a primer for the human immunodeficiency virus region 1, which was used to demonstrate an improved method for synthesising multiple copies of a RNA target sequence. The method comprises combining the target with a primer which hybridises to the 3'-portion of the DNA primer extension prod., reverse transcriptase, RNase I and transcriptase. It can be used as a component of an assay to detect forensic samples. It also has the advantages of being autocatalytic, transcriptase and avoids repetitive manipulations of reaction conditions e.g. temp., ionic strength and pH. (Updated on 25-MAR-2003 to correct pefficial 1) in process.
                                                                                                                                                                                                                                                                                                                                                         Auto-catalytic synthesis of multiple copies of an RNA target sequence - uses cooperative action of a DNA and RNA polymerase in presence of RNase H, useful for detection of target sequence e.g. in clinical or
                                                                                                                                                                                                                                                                                                          Example; Col 9-10; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENP-) GEN-PROBE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus; HIV; region 1; primer; auto-catalytic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ86607-09 are primers and a probe for the human immunodeficiency virus regulon 1. They are used to produce autocatalytic oligonucleotides which require no change in the experimental conditions i.e.constant temperature, pH and ionic strength. These sequences are useful in generating multiple copies of specific nucleic acid target sequences. (Updated on 25-MAR-2003 to correct pF field.)
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16-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunodeficiency virus
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80.8%;
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Pred. No. 1.3e-05
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                                                                                                                This invention describes a novel method for the autocatalytic amplification of an RNA target in a transcription-based amplification system without thermalcycling. The method generates oligonuclectides for cloning. Typical applications are the detection of genetic or infectious diseases, the monitoring of responses to therapy, the quantitation or detection of microorganisms in foods, forensic studies and the provide many copies of selected RNA targets under conditions of constant temperature, ionic strength and ph. Specific amplification of RNA targets increases sensitivity, convenience, accuracy and the reliability of
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Best Local (
                                                                                                Sequence 54
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10-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Autocatalytic amplification; transcription-based amplification; thermalcycling; diagnostic; environmental testing; probe; detection; genetic disease; infectious disease; microorganism; food; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV region 1 primer #1.
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                                                             Similarity
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AATTTAATACGACTCACTATAGGGAGACAAGGGACTTTCCGCTGGGGACTTT
                                                                                                                                                                                                                                                                             autocatalytic amplification of RNA targets
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90US-00550837.
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80.8%;
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                                             Score 36; DB 2; Lo
Pred. No. 1.3e-05;
0; Mismatches 10;
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Pred. No. 1.3e-
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to oligonucleotides useful in amplifying and detecting human immunodeficiency virus (HIV) nucleic acid in a sample. The invention is used for environmental testing, diagnostic testing, research studies and for the preparation of reagents or materials for cloning or other purposes. The present sequence is HIV region specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New oligonucleotide probe, useful in detecting HIV nucleic acid sample and for environmental and diagnostic testing.
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10-JUL-1990;
                                                                                                                     HIV-1 protease
                                                                                                                                                                                                                                                                                                                                                                     Sequence 54
                                                                                                                                                                                                                                                                                                                                                                                              cloning or other PCR primer. This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
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               09-MAY-2002
                                      US2002055095-A1
                                                           Human immunodeficiency virus 1.
                                                                                  HIV; human immunodeficiency virus; ss; primer; gag; pol; protease; reverse transcriptase; infection; PCR.
                                                                                                                                              29-AUG-2003
12-AUG-2002
                                                                                                                                                                                   ABK53107;
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90US-00550837.
95US-00469067.
                                                                                                                      gene specific oligonucleotide primer
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                                                                                                                                                                                                                                                                                                                                                                                            purposes. The pre
sequence is used
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                                                                                                                                               entry)
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80.8%;
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Pred. No. 1.3e-05;
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                                                                                                                                                                                                             HIV-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid oligomers
1 and probes for detecting
pol regions and are useful
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                                                                                                                                                     Enterobacteria phage T7.
                                                                                                                                                                                                                                                                                                                                         AAL45469 standard;
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                                         01-SEP-2000; 2000WO-US024117
                                                                     01-SEP-2000; 2000WO-US024117.
                                                                                                                          WO200220852-A1.
                                                                                                                                                                   Human immunodeficiency virus 1.
                                                                                                                                                                                                                                      HIV-1 pol gene protease amplification oligomer SEQ ID
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GEN-PROBE INC
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76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for amplifying a nucleotide sequence for
the amplified product are specific for
to detect different subtypes of HIV-1.
                                                                                                                                                                                                             PCR; primer; drug resistance; genetic subtype;
                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31.8;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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RESULT 12
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Matches 39
       primers and r
The present invention is concerned with the detection of nucleic acid markers for prostate and breast cancer, and PCR primers and probes which are able to detect and quantify these markers. Prostate specific antigen (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein -2 (hK2) have all been linked to prostate and breast cancers, and the primers and probes of the invention are able to detect the abnormal presence of mRNA expressed by their coding sequences in tissues other
                                                                                                          Detecting prostate-specific antigen (PSA), prostate specific membrane antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using probe molecules, useful for the diagnosis of prostate and breast cancers.
                                                                                                  Claim 1; Page 13;
                                                                                                                                                                                                                                      28-JAN-1999;
                                                                                                                                                                                                                                                           28-JAN-2000;
                                                                                                                                                                                                                                                                                   03-AUG-2000
                                                                                                                                                                                                                                                                                                        WO200044940-A2
                                                                                                                                                                                                                  (GENP-)
                                                                                                                                                                                                                                                                                                                                                            Prostate specific antigen;
glandular kallikrein-2; hK
                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleic acid oligomers which can be used to amplify the gag and pol genes of human immunodeficiency virus type I (HIV-1). These are used to detect regions of the gag and pol genes, especially regions associated with drug resistance, and also for identifying genetic subtypes of the virus. The present sequence is an oligomer of the invention. (Updated on 29-AUG-2003 to standardise os
                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA76206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid oligomer, useful and pol genes of human immune def
                                                                                                                                                                                                                                                                                                                                                    primer; ss
                                                                                                                                                                  2000-505986/45.
                                                                                                                                                                                                                                                                                                                                                                                                prostate
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                                                                                                                                                                                                               GEN-PROBE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTTAATACGACTCACTATAGGGAGACGGCGCCAACCTGCTAGGGATTT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTTÄÄTÄČGÄCTCÄCTÄTÄGGGÄGÄCCACAGCCÄTCCATTCCTGGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug
                                                                                                                                                                                        Clark TJ;
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                                                                                                                                                                                                                                                          2000WO-US002270
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                    99US-0117640P
                                                                                                                                                                                                                                                                                                                                                                                             specific antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistance.
                                                                                              77pp;
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76.5%;
                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                              hK2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babola
                                                                                                                                                                                                                                                                                                                                                                        PSA;
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                                                                                                                                                                                                                                                                                                                                                        3A; prostate-specific membrane antigen; PSMA;
prostate cancer; breast cancer; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31.8; D
Pred. No. 0.00
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             PCR
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                                                                                                                                                                                                                                                                                                                                                                                            primer
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ches 12;
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                                                                                                                                                                                                                                                                                                                                                                                            SEQ
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                                                                                                                                                                                                                                                                                                                                                       breast cancer; probe;
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Matches 35
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Best Local S
Matches 35
                                                                                                The present sequence is a PCR primer used in the amplification of the Mycobacterium avium subsp. paratuberculosis 23S rRNA gene. This gene contains several mutations when compared to other Mycobacterium avium subspecies, and some are unique enough to allow the development of a probe which enables specific identification of the presence of paratuberculosis. The organism is responsible for Johne's disease in runinants, especially cows, and is possibly transmitted to humans where it may lead to Crohn's disease. Efficient detection of the bacterium, using a probe designed using this sequence, can be used to identify infected animals so that they can be removed from the herd and destroyed
                                                                                        Sequence 52
                                                                                                                                                                                                                     Example 1; Fig 6; 81pp; English.
                                                                                                                                                                                                                                        Detection of Mycobacterium avium paratuberculosis pecific 23S rRNA mutations at positions 754, 1363 diagnosis of Johne's disease.
                                                                                                                                                                                                                                                                                                          Schut F, Ensing H2
Brinkhof JMA, Van
                                                                                                                                                                                                                                                                                        WPI; 2000-423446/36.
                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                              03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium avium
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200034517-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium
                                                                                                                                                                                                                                                                                                                                             (GEZO-)
                                                                                                                                                                                                                                                                                                                                                       (MICR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA63315 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johne's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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and a
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                                                         Similarity
ATTCTAATACGACTCACTATAGGGAGAAGGGCTTCACCCTG
               AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTG
                                                                                                                                                                                                                                                                                                                                        GEZONDHEIDSDIENST DIEREN.
                                                                                                                                                                                                                                                                                                                                                    MICROSCREEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease;
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                                           60.4%;
milarity 85.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate. This enables the presence in the detection of metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATTAATACGACTCACTATAGGGAGACTGTGGCTGACCTG
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                                                                                       BP; 15
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Van Maanen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crohn's
                                                                                     A; 12 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
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                                                                                                                                                                                                                                                                                                          Koopmans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.4%;
85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
                                           0
                                                                                    13 G; 12 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       paratuberculosis
                                        Score 31.4; DB 3
Pred. No. 0.0013;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                  PST,
                                                                                 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                 Wagter LHA;
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                                                            Length
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                                         Indels
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                    41
                                                                                                                                                                                                                                                 by identification of or 3093 useful for
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RESULT 14

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RESULT 15
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Matches 33
                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAX26206 to AAX26217 represent claimed oligonucleotides that can be used as primers and probes in the amplification and detection of all subtypes of human immunodeficiency virus type 1 (HIV-1). The oligos are substantially complementary to a sequence of the long terminal repeat (LTR) region of a nucleic acid sequence of a HIV genome. The invention provides a method for detection of HIV-1 nucleic acid using these sequences. Unlike prior art primers and probes, these oligos can detect all known subtypes of HIV-1 with high sensitivity and accuracy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New oligonucleotide primers and probes complementary to the LTR region HIV-1 - useful for amplification and detection of HIV-1 infections.
                                                                                                                                                                                                                                                                                                                                                                     Sequence 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 23; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goudsmit J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligo complementary to LTR region of HIV-1 genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX26214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX26214 standard; DNA; 47
                                                                                         retroviral
                                                                                                                   Primer #1 of the invention.
                                                                                                                                           29-JAN-2004
                                                                                                                                                                       ADE48105;
                                                                                                                                                                                              ADE48105 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-167457/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human immunodeficiency virus type 1; long terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-1; nucleic acid amplification;
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             02-OCT-2003
                                       WO2003080869-A2
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                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                AATTTAATACGACTCACTATAGGGAGACGGGCGCCA 36
                                                                                                                                                                                                                                                              ATTCTAATACGACTCACTATAGGGAGAGGGGGCGCCA
                                                                                         nucleic acid; body fluid; primer;
                                                                                                                                                                                                                                                                                                                                                                     BP; 15 A; 10 C; 13 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oudshoorn
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                                                                                                                                           entry)
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91.7%;
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                                                                                                                                                                                                                                                                                                               Score 31.2; DB 2; Length 47; Pred. No. 0.0015; O; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection; LTR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lukashov VV;
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repeat; ss.
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                                                                                                                                                       The present invention relates to detecting and quantifying a nucleic acid in at least one sample comprising administraring the sample to a solid carrier capable of at least in part absorbing the sample and providing at least a representative part of the carrier to a nucleic acid isolation solution to extract a representative amount of the nucleic acid from the carrier. The method is particularly useful for detecting viral nucleic acid, especially retroviral nucleic acid, in a sample such as a body fluid. The present sequence represents a primer of the invention.
                                                                                                                                                                                                                                                                                                                                              Detecting and quantifying a nucleic acid in a sample, useful for detecting viral RNA, comprises administering the sample to a carrier, exposing the carrier to nucleic acid isolation solution to extract an amount of nucleic acid.
                                                                                                                               Sequence 47 BP; 15 A; 10 C; 13 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-876928/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUL-2002; 2002EP-00077697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUL-2003; 2003WO-NL000491
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                  AATTTAATACGACTCACTATAGGGAGACGGGCGCCA
ATTCTAATACGACTCACTATAGGGAGAGGGGCGCCA
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                                                                             60.0%;
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                                                                             Score 31.2; DB 9
Pred. No. 0.0015;
                                                               Mismatches
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37
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Search completed: August 31, 2004, 01:37:13
Job time: 345.065 secs

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Result
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Maximum Match
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                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Score
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seq length: 100
Query
Match
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2186 71-E9724	218	14	80		۲	41
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4641 012F12 I	3464	13	77	42.7	22.2	37
680645 LmFr1	64	9	73		2	36
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32356 1119	3235	29	100	Ψ	<u>ب</u>	29
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28814 1119	288	29	100	Ü	۲,	26
1807 SWAMCA	180	9	97	43.1	N	25
337 K3123E	337	14	89	·	۲	24
CG728803 1119103C1	CG728803	29	88	ω	۲.	23
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97214 RPC	9721	28	30		N	19
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29055 1119107	N	29	100	S	23.6	17
729011 11191060	2901	29	100	5	Ü	16
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617314 zehn1391	I6173	9	96		u.	14
.I353583 zeh0701.	I3535	9	95	5	w.	13
53162 zeh0113.	3531	9	95		w.	12
G732908 1119152	90	29	90	5	ü	11
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A336070	A33607	14	79	5	ü	9
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16894 zehn0783.	1616894		96	7.	٠	7
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CG732206 1119146G0	G73220		90	80		ஶ

ALIGNMEN:

JOURNAL MEDLINE PUBMED COMMENT REFERENCE AUTHORS SOURCE ORGANISM VERSION KEYWORDS RESULT 1 AJ282930 DEFINITION ACCESSION rocus TITLE AJ282930 79 DP MKNA 4A3A-P1E1-R Anopheles gambiae immune compete gambiae cDNA clone 4A3A-P1E1, mRNA sequence. Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,
Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
and Kafatos,F.C. Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000) Anopheles gambiae (African malaria mosquito) Anopheles gambiae Eukaryota, Metazoa; Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Contact: Dimopoulos G Fotis C. Kafatos laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany. EST AJ282930.1 GI:6930809 10841561 (bases 1 to 79) op mRNA linear EST 30-JUN-2000 immune competent 4A3A Anopheles

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25.6 25.6 25.4

50.0 49.2 48.8

79 100 100 87

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AJ282930 AI353756 CG728851 CA406952

AJ282930 4A3A-P1E1 AI353756 zeh0940.s CG728851 1119104C1 CA406952 1003101 H

FEATURES

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AI353756/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                         PCR PRIMETS

PCRWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTGACCCTCACTAAAGGG 3'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 6179750995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 100)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zeh0940.seq.F Zebrafish
cDNA 5', mRNA sequence.
AI353756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                             cliew@rics.bwh.harvard.edu
             /dev_stage="embryonic day 3 post-fertilization"
/lab host="E.coli XL1-Blue mrr'"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/clone_Typan: heart; Vector: Lambda ZAP Express; Site_1:
EcoRI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
                                                                                                                                                                                                /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Clone lib="Anopheles gambiae immune competent 4A3A"
/note="Wector: pTTT3D-Rac (Pharmacia) with a modified
polylinker; Site=1: EcoRI; Site=2: NotI; sequenced from
forward priming site which reads from the 3' end of the
CDNA. The 4A3A is a directionally cloned and normalized
CDNA library that was constructed from the 4A3A cell line
cligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996): Normalization and Subtraction: Two approaches To
Pacilitate Gene Discovery, Genome Research 6, 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell line="immune competent 4A3A"
/lab_host="E_ coli DH10B"
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/clone="4A3A-P1E1"
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directional cloning into pre-digested lambda ZAP
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85.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dempsey, A.A., Hwang, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp mRNA linear EST 04-JAN-19
Embryonic Heart cDNA Library Danio rerio
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Ostariophysi;
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CG728851
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             29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           survey sequence.
CG728851
CG728851.1 GI:37
GSS.
Zea mays
                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
ATTGTAATACGACTCACTATAGGGCGATTTGCGGCAGCACGGCGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reverse complemented post-ligation sequence from source sequence. Plate: 1119104 row: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Very probable ligation site of ends cut by single endonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanford University
                                AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize genomic sequences found using engineered RescueMu transposon
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                                                                           Conservative
                                                                                                                                             / Ann_________/ Clone lib="119 - RescueMu Grid AA"
/ Clone lib="119 - RescueMu Grid ABMHI, Site_2: BgIII,
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
Was extracted from laef strips, double digested using
DH10B cells were transformed and then screened on LB
plates with ampicillin."
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                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/cultivar="mixed_background_W23/A188/B73/K55"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="leaf"
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70.8%;
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                                                                     Score 25.6; DI
Pred. No. 20;
0; Mismatches
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Pred. No. 20
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Zea mays genomic, genomic
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1119146G02.1EL_x1 1119 -
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Fax: 410 706 1622
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Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St, HH497, Baltimore, MD 21201, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang,R.-Z., Shuldiner,A. and Gong,D.-W.
EST analysis of human adipose gene expression
Unpublished (2002)
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cDNA 5', mRNA sequence.
CA406952
CA406952.1 GI:24771823
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Seq primer: GTTGGTACCCGGGAATTC.
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                                                                                                          Contact: Walbot V
Department of Biological Sciences
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Email: walbot@stanford.edu
Very probable ligation site of enda
Reverse complemented post-ligation
                                                                                           Stanford University
                                                                                                                                                                     Walbot, V.
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                                                                              855 California Ave, Palo
                                                                                                                                           Unpublished (2001)
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650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male and Female"
/tissue_type="Adipose"
/clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
/note="Vector: lambdaTriplEx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Eutheria, Primates, Catarrhini, Hominidae,
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Pred. No. 22;
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 s cut by single endonuclease. sequence from source sequence
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Zea mays
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Class:
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                                                                                                                                                                                                                                                                    Stanford University
855 California Ave, Palo Al
855 California Ave, Palo Al
Tel: 650 725 8221
Fax: 650 725 8221
Email: walbot@stanford.edu
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                            Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Walbot
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Unpublished (2001)
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CG729102
CG729102.1 GI:3
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/clone lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
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/dev_stage="adult"
/lab_host="DH108"
/clone_lib="1119 - F
                                                                              /organism="Zea mays"
/mal_type="genomic DNA"
/cultivar="nixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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                                                            tissue_type="leaf"
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Best Local S
Matches 33
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A1616894/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                   POR Primers
FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Sed primer: 5' GAAATTAACCCTCACTAAAGGG 3'

                              h 47.3%;
Similarity 70.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115,
Tel: 6177328915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 96)

Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AATTTAATACGACTCACTATAGGGAGACGGGGGGCCAAC 38
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AI616894.1 GI:4626061
EST.
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             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cliew@rics.bwh.harvard.edu
                                                                                                   /dew_stage="embryonic day 3 post-fertilization"
/lab host="E coli XLI-Blue mrF'"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: Lambda ZAP Express; Site 1:
RCORI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector. "
                                                                                                                                                                                                                                                                                                                       /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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        Score 24.6; D: Pred. No. 47; 0; Mismatches
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Pred. No. 28;
O; Mismatches
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Heart cDNA Library Danio rerio
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        14;
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                                              Length 96;
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CA336070/c
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AI087772/c
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                                                                                                                                                                                                        67
                                         CA336070 79 bp mRNA linear EST 04-NOV-2002 INJECT 1007h08.yl COGENE 4AR (4EAR) Homo sapiens cDNA clone IMAGE:5607422 5', mRNA sequence.
CA336070
CA336070.1 GI:24554168
EST.
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                                                                                                                                                                                                                                                                                        25;
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AI087772
AI087772.1 GI:3426748
BST.
Onchocerca volvulus
Onchocerca volvulus
Conchocerca, Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Conchocercidae; Onchocerca.
1 (bases 1 to 75)
1 (bases 1 to 75)
                                                                                                                                                                                                                                                                                                       Similarity
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01083, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lizotte-Waniewski,M. and Williams,S.A.
Genes expressed in adult male stage of Onchocerca volvulus
Unpublished (1998)
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
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75 bp mRNA linear EST 18-AUG-19: SWOVAMCAQO2F02SK Onchocerca volvulus adult male cDNA (SAW98MLM-OVAM) Onchocerca volvulus cDNA clone SWOVAMCAQO2F02 5',
                                                                                                                                                                                                  AATGTAATACGACTCACTATAGGGCGA 41
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                                                                                                                                                                                                                                                                                 45.8%;
ilarity 92.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Filarial nematode parasite of humans. Six adult male worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult male mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2 x 10E5 independent recombinants and the average insert size is ~1100bg. The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr. Steven A. Williams, email: genome@smith.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvAMCAQ02F02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev stage="adult"
/lab_host="XL1-Blue MRF'"
/clone lib="Onchocerca volvulus adult male cDNA
(SAM98MLM-OvAM)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Onchocerca
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                     Score 23.8;
Pred. No. 87;
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                                                                                                                                                                                                                                                                                                                     Length 75;
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RESULT 10
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Zea mays
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                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Seq primer: M13RP1 reverse primer
Location/Qualifiers
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Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                         Stanford University
855 California Ave, Palo
                                                                                                                                                                                                                                                                                                                                                                                            1119160E10.1EL_x1 1119 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                  Department of Biological Sciences
                                                                                                                      Contact: Walbot V
                                                                                                                                      Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                    CG733887
CG733887.1
                                                                                                                                                                                                                                                                                                                                                                           survey sequence.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                             Walbot, V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTAATACGACTCACTATAGGGAGACG 29
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                                                                                                                                                                                                (bases 1 to 86)
650 723 2227
650 725 8221
l: walbot@stanford.edu
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/dev_stage="embryo, 4 weeks postconception"
/lab_host="bH10B"
/clone_lib="COGENE 4AR (4EAR)"
/clone_lib="COGENE 4AR (4EAR)"
/note="Vector: pAMP1; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of pAMP1. Size
selected for insert sizes ranging from 0.3-1.6 kb.
Normalized to Cotl0. Primary library, non-amplified.
Library constructed by M. Lovett. For moore information on
this library, please contact R. Tidwell (Washington
University) or visit the COGENE website at
http://hg.wustl.edu/COGENE/."
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/db_xref="taxon:9606"
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/mol_type="mRNA"
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Pred. No. 89;
                                                           Alto,
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                                                           CA 94304, USA
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TITLE
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                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 45.4%;
Local Similarity 76.3%;
nes 29; Conservative
                                                                                                                                                              Stanford University
855 California Ave, Palo Alto, CA 9430
7e1: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cu
Reverse complemented post-ligation sec
Plate: 1119152 row: 14
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                                                                                                                                             Class: transposon-tagged
                                                                                                                                                                                                                                                                                                                                 Department
                                                                                                                                                                                                                                                                                                                                                    Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                       Maize genomic sequences found using Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                Walbot, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG732908.1
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGTAATACGACTCACTATAGGGCGATTTGCAGCAGC 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Clone_lib="1119 - RescueMu Grid AA"
//Clone_lib="1119 - RescueMu Grid AA"
//note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site_2: BgIII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BgIII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
/mol_type="genomic_DNA"
/cultivar="mixed_background_W23/A188/B73/K55"
/db_xref="taxon:4577"
/tiBsue_type="leaf"
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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/lab_host="DH10B"
                                                                                 organism="Zea mays"
                                                                                                                     ocation/Qualifiers
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Pred. No. 1.1e+02;
0; Mismatches 9
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Grid
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sequence from source sequenc
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; Poales; Poaceae;
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aceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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VERSION
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AI353162/c
LOCUS
                        Query Match
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Best Local S
Matches 29
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                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115,
Tel: 6177328915
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Liew, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cliew PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 6179750995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinopterygii; Neopterygii; Tele
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 95)
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EST.
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                                                                            /organism="Danio rerio"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:7955"
/dev_stage="embryonic day 3 post-fertilization"
/lab_host="E_coli XL1-Blue mrF'"
/clone lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1: XhoI; mRNA was purified from embryonic zebrafish hearts (3 day post-fertilization). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional clonning into pre-digested lambda ZAP
Express vector. "
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamWif, Site_2: BglII; RescueMu is a 4.9 kb, modified maker Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.isstate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with amnicillar "
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              45.4%;
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         Score 23.6;
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Pred. No. 1.1e+02;
0; Mismatches 9; Indels
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Embryonic Heart cDNA Library Danio rerio
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         BB
9;
    Length 95;
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AI617314/c
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Matches 32
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AUTHORS
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AI353583/c
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                                               AI617314
zehn1391.
cDNA 5',
AI617314
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   Danio rerio
                               AI617314.1
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                                                                                                                                                                                                                                                                 Similarity
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Harvard Medical School
75 Francis St. Boston, MA 02115,
Tel: 6177328915
Fax: 6179750995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
Contact: Liew CC
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zeh0701.seq.F Zebrafish
cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                            /organism="Danio rerio"
/mol_type="mRNA;"
/db_xref="taxon:7955"
/db_xref="taxon:7955"
/dev_stage="embryonic day 3 post-fertilization"
/lab_lost="E.coli XL1-Blue mrF'"
/clone lib="Zebrafish Embryonic Heart cDNA Library"
/clone lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: Lambda ZAP Express; Site 1:
ECCRI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloming into pre-digested lambda ZAP
Express vector. "
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                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
(zebrafish)
                               GI:4626481
                                                                                                                                                                                                                                                              45.4%;
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                                                                                                                                                                                                                                            Score 23.6; DB 9;
Pred. No. 1.1e+02;
0; Mismatches 14;
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Embryonic
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D; Mismatches 14;
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Embryonic Heart cDNA Library
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Heart
                                                                       cDNA Library Danio rerio
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                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 96)
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zehl1725 Zebrafish Embryonic Heart
5', mRNA sequence.
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                                       Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02
Tel: 6177328915
                                                                                                                       an Embryonic Zebrafish
Unpublished (1999)
Contact: Liew CC
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FORWARD: 5' GCCAAGCTCGAAATTAACCCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
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Harvard Medical School
75 Francis St. Boston, MA 02115, USA
                                                                                                                                                                                                                              Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M.,
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cliew@rics.bwh.harvard.edu
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/lab_host="E.coli XL1-Blue mrf'"
/clone lib="Zebrafish Embryonic Heart cDNA Library"
/clone rogan: heart; Vector: Lambda ZAP Express; Site_1:
EccRI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dr adaptor primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector. "
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/mol_type="mRNA"
/db_xref="taxon:7955"
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Pred. No. 1.1e+02;
0; Mismatches 14;
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  TGTAATACGACTCACTATAGGGCGAATTGGGTACACTTACCTGGTA 51
                            TTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGA 48
                                                                                 Conservative
                                                                                                                                                                                     /dev_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue mrp"
/clone lib="Zebrafish Embryonic Heart cDNA Library"
/note="Togan: heart; Vector: Lambda ZAP Express; Site_1:
EcoRI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-oligo dT adaptor; primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector. "
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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                                                                                                        45.4%;
                                                                                    0;
                                                                                                        Score 23.6; DB 10;
Pred. No. 1.1e+02;
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Search completed: August 31, 2004, 03:09:42
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is derived by analysis of the total score
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Maximum Match 100%
Listing first 45 summaries
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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-168-947-26
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8-482-428-14 8-486-705-14 9-944-036-3 9-944-036-3 8-360-051A-23 8-360-051A-23 9-202-972-16 8-633-122-3 8-633-122-3 8-631-12-3 8-631-12-3 8-631-12-3 8-631-12-3 8-631-12-3 8-631-12-3 8-631-12-3 8-631-12-3 8-631-12-3 8-631-12-2 8-683-122-2	096		r	_	1	_	Н	_	4	4	_	_	_	-	Н	4	N	4	Н	1
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14, Appl 14, Appl 23, Appl 23, Appl 16, Appl 3, Appl 3, Appl 4, Appl 4, Appl 7, Appl 7, Appl 7, Appl 7, Appl 8, Appl 17, Appl 17, Appl 17, Appl 18, Appl 19, Appl 19, Appl 19, Appl 19, Appl 2, Appl 2, Appl 2, Appl 2, Appl 3, Appl 10, Appl 11, Appl 11, Appl 12, Appl 12, Appl 12, Appl 12, Appl 13, Appl 14, Appl 15, Appl 16, Appl 17, Appl 18, Appl 19, Appl					Sequence													Sequence		
Appl Appl Appl Appl Appl Appl Appl Appl			•				-		•	•	-	•	•	•	•	16,	23,	ω.		14,
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CURRENT APPLICATION NUMBER: US/09/611,627
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/143,072
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 50
                                                                                                                                                                                                                                           RESULT 2
US-09-611-627-26
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GENERAL INFORMATION:
APPLICANT: BEE, Gary G.
APPLICANT: YANG, Yeasing Y.
APPLICANT: KOLK, Dan
APPLICANT: KOLK, Dan
APPLICANT: GIACHETTI, Cristina
APPLICANT: McDONOUGH, Sherrol H.
APPLICANT: MCDONOUGH, Sherrol H.
TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
FILE REFERENCE: GP103-02.UT
CURRENT APPLICATION NUMBER: US/09/611,627
                                                                                                                                                                                                   Sequence 26, Application Patent No. 6623920
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TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
FILE REFERENCE: GP103-02.UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amplification oligomer with 5' promoter sequence, OTHER INFORMATION: for HIV-1 LTR region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 1.1e-06;
D; Mismatches 1
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CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/14:
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 57

60/143,072

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RESULT 4
US-09-944-036-7
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COURRENT FILING DATE: 1998-10-08
FARLIER APPLICATION NUMBER: 08/469,067
FARLIER FILING DATE: 1995-06-06
FARLIER FILING DATE: 1995-07/550,837
FARLIER FILING DATE: 1990-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FREUSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
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  APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABCIA, Odile
APPLICANT: BABCIA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: SMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP114-02.UT
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Best Local Similarity
Matches 42; Conserv
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CURRENT APPLICATION NUMBER: US/09/944,036
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APPLICANT: FULTZ, TIMOTHY J.
APPLICANT: MCDONOUGH, SHERROL H.
TITLE OF INVENTION: DETECTION OF HIV
FILE REFERENCE: 218/130
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SEQ ID NO 26
ENGTH: 51
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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80.8%;
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94.2%;
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Pred. No. 1.6e-06;
0; Mismatches 10
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Pred. No. 1.1e-06;
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US-09-493-491A-38
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Patent No. 6551778
GENERAL INFORMATION:
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US-09-493-491-35
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APPLICANT: HARVEY, Richard, C.
APPLICANT: CLARK, JR., Thomas, J.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING
TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
FILE REFERENCE: GP097-02.UT
CURRENT APPLICATION NUMBER: US/09/493,491A
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/117,640 US
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 7
SEQ ID NO 8
SEQ ID
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SOFTWARE: PatentIn Ver.
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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APPLICANT: HARVEY, Richard, C.
APPLICANT: CLARK, JR., Thongs, J.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
FILE REFERENCE: GP097-02.UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/493,491
CURRENT FILING DATE: 2000-01-28
EARLIER APPLICATION NUMBER: 60/117,640 US
EARLIER FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6391
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Best Local Similarity

Matches 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.4%; Score 31.4; DB 4;
85.4%; Pred. No. 0.00016;
tive 0; Mismatches 6
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Pred. No. 0.00011;
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                                                                                                                                                                            GENETIC MARKERS
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PRIOR FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1

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                                                                                                                                                                                                                                       US-09-944-036-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KACIAN, DANIEL L.
APPLICANT: FULTZ, TIMOTHY J.
APPLICANT: MCDONOUGH, SHERROL H.
TITLE OF INVENTION: DETECTION OF HIV
FILE REFERENCE: 218/130
CURRENT APPLICATION NUMBER: US/09/168,947
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 08/469,067
EARLIER FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 07/550,837
EARLIER APPLICATION NUMBER: 07/550,837
EARLIER FILING DATE: 1990-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                            Sequence 5, Application US/09944036 Patent No. 6582920
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Best Local S
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APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
APPLICANT: VERNET, Guy
APPLICANT: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: promoter LOCATION: (1)..(28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 49
TYPE: DNA
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70. 6589734
                                                                                                                                                                              INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                           h 58.5%;
Similarity 85.0%;
34; Conservative
                                                                                                                                                                                                                                                                                                                AATTTAATACGACTCACTATAGGGAGAGGGGTGGCTCCTT 40
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Pred. No. 0.00016;
0; Mismatches 6
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RESULT 10
US-09-040-220D-7
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Sequence 7, Application US/09040220D
Patent No. 6391311
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 37
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Patent No. 6582920
GPNPDA**
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Best Local (
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENUET, GUY
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligonucleotide primer for Gag target sequence NAME/KEY: promoter LOCATION: (1)..(29)
                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligonucleotide primer for Protease target OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: promoter LOCATION: (1)..(33)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
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                                                                                                                                                                                                                                                                                         58.1%;
74.5%;
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Pred. No. 0.00052;
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Pred. No. 0.00052
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CURRENT APPLICATION NUMBER: US/09/265,686
CURRENT EILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
INDIANG OF SEQ ID NOS: 8
                                                                                                                                             RESULT 12
US-09-723-749-7
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US-09-265-686-7
; Sequence 7, Application US/09265686
; Patent No. 6455283
                                                                                                                                                                                                                                                                                                                                                         US-09-265-686-7
                Sequence 7, Application US/09723749
Patent No. 6620784
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND EMPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-48
OTHER INFORMATION: Sequence is synthesized
Patent NO. 6455283
                                                                                                                                                                                                                                                                                                         Query Match
Best Local
CURRENT APPLICATION NUMBER: US/09/723,749
                                                                                                                                                                                                                                                                                        Matches
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NAME/KEY: Artificial
LOCATION: 1-48
OTHER INFORMATION: Sequence is synthesized
Patent No. 6391311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ferrara, Napoleone APPLICANT: Kuo, Sophia S. TITLE OF INVENTION: POLYPEPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                      AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTG 41
                                                                                                                                                                                                      ATTCTAATACGACTCACTATAGGGCGGCGGAATCCAACCTG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTG 41
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iilarity 82.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
                                                                                                                                                                                                                                                                                                 57.3%;
82.9%;
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                                                                                                                                                                                                                                                                           Score 29.8; DB 4;
Pred. No. 0.00076;
0; Mismatches 7
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Pred. No. 0.00076;
                                                                                                                                                                                                                                                                                                           DB 4; Length 48;
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                                                                                                                                                                                                                                                                         7; Indels
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CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 09/265,686
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-162-836-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: Artificial
LOCATION: 1-48
OTHER INFORMATION: Sequence is synthesized
Patent No. 6620784
                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                             TELEPHONE: (213) 489-1600
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,836
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Daniel L. Kacian
APPLICANT: Diane L. McAllister
APPLICANT: Sherrol H. McDonough
APPLICANT: Nani Bhushan Dattagupta
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION
TITLE OF INVENTION: METHOD, COMPOSITION AND KIT
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                  TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                       NAME: Warburg, Richard
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM compatible OPERATING SYSTEM: IBM P.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: LOB Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTG 41
                                                                                                           67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J, Application US/08162836
5554516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Lyon & Lyon
611 West Sixth Street
                                                                                                                               (213) 955-0440
linear
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                                                                                                                                                                                                    32,327
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Pred. No. 0.00076
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RESULT 15
US-08-479-105A-6
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                                                                                                                                                                                                                                               US-08-345-861-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Approximately No. 5766849
Sequence 6, Application US/08479105A Patent No. 5908744 GENERAL INFORMATION:
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                           TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5766849 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OFERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATE: 07/9:
APPLICATION UNMBER: 07/9:
FILING DATE: August 4, 1:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 197/136
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thomas B. Ryder
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 611 West S
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (613) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM COMPONER SYSTEM:
                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                AATTTAATACGACTCACTATAGGGAGACCAGGCCACTTCCGCTA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08345861
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611 West Sixth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nanibhushan Dattagupta
Diane L. McAllister
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Philip Hammond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Daniel L. Kacian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherrol H. McDonough
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79.5%;
                                                                                                                                                                                             56.9%; Score 29.6; DB 1; 79.5%; Pred. No. 0.00092;
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Search completed: August 31, 2004, 04:43:18 Job time: 82.7143 secs
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                                                                                                                                         Matches
                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/925,405
FILING DATE: August 4, 1992
APPLICATION NUMBER: 07/855,732
FILING DATE: MARCh 19, 1992
APPLICATION NUMBER: 07/550,837
FILING DATE: July 10, 1990
APPLICATION NUMBER: 07/379,501
FILING DATE: July 11, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon 0.
REGISTRATION NUMBER: 38,179
REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 47 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Diane L. McAllister
APPLICANT: Philip Hammond
TITLE OF INVENTION: NUCLEIC ACID
TITLE OF INVENTION: AMPLIFICATION
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/479,105;
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,861
FILING DATE: No. 5908744ember 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect | CURRENT APPLICATION DATA:
                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                            LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 633 West I
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPACIE
OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                   90071-2066
                                                                                                                                                                                                                                                                                                                                       67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             633 West Fifth
                                                                                                                                                                                                                                                                                                                                                        (213) 955-0440
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WordPerfect 5.1
                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.5" Diskette, 1.44 Mb
                                                                                                                                                       56.9%;
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                                                                                                                                       Score 29.6; DB 2;
Pred. No. 0.00092;
n: Mismatches 9;
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Minimum |
Maximum |
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB seq length: 0
DB seq length: 100
                                                                                                                               Published Applications NA:*

1: /cgm2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgm2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgm2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgm2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgm2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

6: /cgm2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

10: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

11: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

12: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

13: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

14: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

15: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

16: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

17: /cgm2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgm2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgm2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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36 36 36 31 30 30 30 30 30 30 30	Score
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5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	% Query Match Length
133 133 134 135 136 137 137 137 137 137 137 137 137 137 137	BB
US-10-001-407-15 US-10-461-790-100 US-10-632-658-8 US-10-001-407-17 US-10-632-658-26 US-10-244-490-2 US-09-944-036-7 US-10-273-707-38 US-10-244-490-15 US-09-944-036-5 US-09-944-036-5 US-09-944-036-37 US-10-425-975-37	ID
Sequence 15, Appl Sequence 8, Appli Sequence 17, Appli Sequence 17, Appli Sequence 26, Appli Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 37, Appli	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15
28	28	28	28	28	28	28	28.2		28.2	28.2	28.2	28.4	28.4	28.4	28.4		28.4	28.6	æ	28.8	28.8	28.8	29	29.2	29.2	29.4	9	29.6	9	9
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49	48	48	45	35	2	N	Q	w	ω	_	8	_	7	w	51	45	39	54	50	50	49	48	55	47	45	47		Ş		48
15	14	9	13	9	16	9	15	15	15	15	14	15	14	15	13	13	15	13	16	9	13	13	<u>1</u> 3	15	5	13	13	13	15	15
US-10-244-490-5	US-10-075-579-7	US-09-975-408-7	US-10-461-790-47	US-09-202-972-16	US-10-425-975-3	US-09-944-036-3	US-10-231-843-7	US-10-231-843-25	US-10-231-843-3	US-10-244-490-25		US-10-077-383-18	US-10-001-407-18	US-10-231-843-5	US-10-363-852-2	-10-461	US-10-077-383-25	US-10-461-790-38	US-10-425-975-8	US-09-944-036-8	US-10-632-658-28	US-10-632-658-24	US-10-461-790-116	-10	US-10-244-490-39	US-10-461-790-39	US-10-461-790-48	US-10-461-790-36	US-10-231-843-9	US-10-178-442-7
Sequence 5, Appli	,	7, A	Sequence 47, Appl	,	Sequence 3, Appli	Sequence 3, Appli	7, 7	25,	Sequence 3, Appli	e 25,	e 42,	θ,	e 18,	<u>ა</u>	'n	49,	25,	38,	Sequence 8, Appli	8, 7	28,	`	e 116	e 2, 1	е 39,	e 39,	e 48,	е 36,	e 9,	

ALIGNMENTS

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RESULT 1

US-10-001-407-15

Sequence 15, Application US/10001407

Publication Mo. US/20020177127A1

GENERAL INFORMATION:

APPLICANT: Wang, Yeasing
APPLICANT: DIVENTION: Terrie
APPLICANT: DIVENTION: Human Immunodeficiency Virus 2 (HIV-2)

FILE REFERENCE: GP117-03.UT

CURRENT FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: 60/242,620

PRIOR PILLING DATE: 2001-03-30

PRIOR PILLING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 15

FEATURE: 52

TYPE: DNA

ORGANISM: Artificial Sequence
FOTHER INFORMATION: primer sequence
OTHER INFORMATION: primer sequence
OTHER INFORMATION: primer sequence

OTHER INFORMATION: primer sequence

US-10-001-407-15

Query Match

Date: 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AATTTAATACGACTCACTATAGGGAGACGGGCCAACCTGCTAGGGATTTT 52

AATTTAATACGACTCACTATAGGGAGACGGGCCAACCTGCTAGGGATTTT 52

Indels 0;

AATTTAATACGACTCACTATAGGGAGACGGGCCCAACCTGCTAGGGATTTT 52
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US-10-461-790-100

Publication No.

Application US/10461790 . US20040029111A1

INFORMATION:

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FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amplification oligomer with 5' promoter sequence; OTHER INFORMATION: for HIV-1 LTR region

US-10-632-658-8
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/632,658
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US/09/611,627
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/143,072
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATENTIN Ver. 2.0
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                                                   Query Match
Best Local Similarity
As. Conserv
                                                                                                                                                                                                                                                                                                    SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/389,393
PRIOR FILING DATE: 2003-06-13
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 142
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 100
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10632658
Publication No. US20040053223A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BEE, Gary G.
APPLICANT: YANG, Yeasing Y.
APPLICANT: KOLK, Dan
APPLICANT: GIACHETTI, Cristina
APPLICANT: GIACHETTI, Cristina
APPLICANT: MCDONOUGH, Sherrol H.
TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
FILE REFERENCE: GP103-02.UT
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Best Local :
                                                                                                                                                                                                                              LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yoshimura, Tadashi
APPLICANT: Ho-Sing-Loy, Marcy
APPLICANT: Stringfellow, Leslie A.
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Hepatitis B Virus
FILE REFERENCE: GP134-02.UT
CURRENT APPLICATION NUMBER: US/10/461,790
CURRENT FILING DATE: 2003-06-13
DRICE APPLICATION TERMS 2003-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Linnen, Jeffer APPLICANT: Kolk, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTTT 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dockter,
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                                                                   70.0%;
94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.0%; Score 36.4; DB 13; 94.2%; Pred. No. 4.7e-06;
                                               <u>.</u>
                                                            Score 36.4; DB 13;
Pred. No. 4.7e-06;
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                                               Mismatches
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                                                                                Length
                                           Indels
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                                    Gaps
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APPLICANT: YANG, Yeasing Y.
APPLICANT: KOLK, Dan
APPLICANT: KOLK, Dan
APPLICANT: GIACHETTI, Cristina
APPLICANT: GIACHETTI, Cristina
APPLICANT: MCDONOUGH, Sherrol H.
TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
FILE REFERENCE: GP103-02.UT
CURRENT APPLICATION NUMBER: US/10/632,658
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US/99/611,627
PRIOR APPLICATION NUMBER: US/09/611,627
PRIOR APPLICATION NUMBER: 60/143,072
PRIOR FILING DATE: 2000-07-09
NUMBER OF SE0 ID NOS: 57
SOFTMARE: Patentin Ver. 2.0
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GENERAL INFORMATION:

APPLICANT: Burrell, Terrie

ITILE OF INVENTION: Compositions and Methods for Detecting

TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)

FILE REFERENCE: GP117-03.UT

CURRENT APPLICATION NUMBER: US/10/001,407

CURRENT FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: 60/242,620

PRIOR APPLICATION NUMBER: 60/242,620

PRIOR APPLICATION NUMBER: 60/280,058

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 34

SOPTWARE: FastSEQ for Windows Version 3.0
                                                                            US-10-632-658-26
                                                                              SEQ ID NO 26
LENGTH: 51
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: amplification oligomer with 5' promo
OTHER INFORMATION: for HIV-1 LTR region
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US-10-001-407-17
US-10-001-407-17
Sequence 17, Application US/10001407
Publication No. US20020177127A1
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BEE, Gary G.
APPLICANT: YANG, Yeasin
APPLICANT: KOLK, Dan
APPLICANT: GIACHETT, C
APPLICANT: MCDONOUGH, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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FEATURE:
CTHER INFORMATION: T7 promoter primer having a promoter sequence
OTHER INFORMATION: appended at the 5' end of the sequence given as
CTHER INFORMATION: SEQ ID NO:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/10632658
No. US20040053223A1
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       70.0%;
94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.0%; Score 36.4; DB 14; Length 94.2%; Pred. No. 4.7e-06; tive 0; Mismatches 1; Indels
Score 36.4; DB 13; Pred. No. 4.7e-06;
                                                                                                         ence: synthetic
promoter sequence,
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Length 51;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthesized nucleic acid molecule 
US-10-244-490-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09944036 Patent No. US20020055095A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10244490 Publication No. US20030152916A1
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                                                                                                                                                                                           SEQ ID NO 7
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                                                                                                                                                                                                      APPLICANT: VERNET, GUY
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIC
FILE REFERENCE: GP114-02. UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR APPLICATION NUMBER: US 60/229,790
RIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/469,067
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/550,837
PRIOR FILING DATE: 1990-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/244,490
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US/09/168,947
PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YANG,
APPLICANT: BRENT
APPLICANT: BABOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MCDONOUGH, SHERROL H. TITLE OF INVENTION: DETECTION OF HIV FILE REFERENCE: 218/130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KACIAN,
APPLICANT: FULTZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 54
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonuclectide primer for Protease target
OTHER INFORMATION: Sequence
NAME/KEY: promoter
LOCATION: (1)..(32)
                                                                                                                        LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        BRENTANO, Ste
                                                                                                                                                                                                                                                                                                                                                                                                                     TRAN, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steven
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7.2e-06;
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US-10-273-707-38
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                                                    GENERAL INFORMATION:
APPLICANT: HARVEY, Richard, C.
APPLICANT: CLARK, JR., Thomas, J.

TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
FILE REFERENCE: GP097-03.DV1
CURRENT APPLICATION NUMBER: US/10/273,707
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 09/493,491
PRIOR FILING DATE: 2000-01-28
PRIOR PELING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-28
PRIOR FILING DATE: 1999-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 7
LENGTH: 52
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Best Local Similarity
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TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIC
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/10/425,975
CURRENT FILING DATE: 2003-04-28
REIOR APPLICATION NUMBER: US/9/944,036
PRIOR PELING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YANG, APPLICANT: BRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonuclectide primer for Protease target
OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: promoter LOCATION: (1)..(32)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
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BABOLA, Odile
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76.5%;
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Pred. No. 0.00053;
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Pred. No. 0.00053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
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US-09-944-036-5
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PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 08/469,067
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/550,837
PRIOR FILING DATE: 1990-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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; LOCATION: (1)..(28)
US-10-273-707-38
  APPLICANT: YANG, YEARING Y.
APPLICANT: BARBYTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT APPLICATION NUMBER: US/09/944,036
                                                                                                                                                                                                              Sequence 5, Application US/09944036 Patent No. US20020055095A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/229,790
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LENGTH: 52
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Best Local Similarity 85.4%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 218/130
CURRENT APPLICATION NUMBER: US/10/244,490
CURRENT FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FULTZ, TIMOTHY J.
APPLICANT: MCDONOUGH, SHERROL H.
TITLE OF INVENTION: DETECTION OF HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KACIAN, DANIEL L. APPLICANT: FULTZ, TIMOTHY J APPLICANT: MCDONOUGH, SHERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthesized nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
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ilarity 85.0%;
Conservative
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Pred. No. 0.0022;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15;
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APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, GUY
ITILE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
ITILE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
CURRENT APPLICATION NUMBER: US/10/425,975
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US/99/944,036
PRIOR APPLICATION NUMBER: US/99/944,036
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN Ver. 2.1
                                           RESULT 13
US-09-944-036-37
US-09-944-036-37
; Sequence 37, Application US/09944036
; Patent No. US200220055095A1
; GENERAL INFORMATION:
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US-10-425-975-5
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US-09-944-036-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: YANG, Yeasing Y.
APPLICANT: BREWTANO, Steven
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
                                                                                                                                                                                                                                                                      Matches
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Best Local (
APPLICANT: YANG, YEASING APPLICANT: BRENTANO, Ste-APPLICANT: BABOLA, Odile
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
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ORGANISM: Artificial Sequence
FEATURE:
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32; Conserv
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                                   Yeasing Y.
                                                                                                                                                                                                                                                                                58.1%;
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Pred. No. 0.0027;
0; Mismatches 3;
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Pred. No. 0.0027;
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PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 53
TYPE: DNA
ORDERS OF SEQUENCE
FEATURE:
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Best Local S
Matches 38
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PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 53
TYPE: DNA
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APPLICANT: YANG, YEA
APPLICANT: BRENTAN
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TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIC
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/10/425,975
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TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US/09/944,036
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                 FEATURE: promoter LOCATION: (1)..(33)
                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligonucleotide primer for Protease target OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38:
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                                                                                             Similarity
                                 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTGCTAGGGATTT
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BABOLA, Odile
TRAN, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAN, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                           Conservative
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74.5%;
                                                                                           58.1%;
                                                                       Score 30.2; DB 16; Length Pred. No. 0.0027; O; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30.2; DB 9; Length Pred. No. 0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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 52
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                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 11669.112USD2
CURRENT APPLICATION NUMBER: US/10/178,442
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 09/265,686
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                     SOPTWARE: PatentIn version 3.1 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10178442 Publication No. US20030113870A1 GENERAL INFORMATION:
                                                                                                Query Match
Best Local Similarity
                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND
                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                 TYPE: DNA
                                                                              34;
                                      1 AATTTAATACGACTCACTATAGGGAGACGGGCGCCAACCTG
ATTCTAATACGACTCACTATAGGGCGGCGGAATCCAACCTG
                                                                              Conservative
                                                                                                  57.3%;
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                                                                                                Score 29.8;
Pred. No. 0.
                                                                                 Mismatches
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                                                                                                                       Length
  43
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Search completed: August 31, 2004, 06:17:10 Job time: 3797.92 secs

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